Supplementary Information Appendix for

Structural basis for Acinetobacter baumannii biofilm formation

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SI Materials and Methods

Bacterial strains and plasmids. Characteristics and source of the bacterial strains used in this study are given in Supplementary Table S1. Oligonucleotides are listed in Supplementary Table S2.

The *Csu* gene cluster was amplified by PCR from chromosomal DNA of *Acinetobacter baumannii* Bouvet and Grimont (ATCC[®] 19606D-5TM) using primers CsuABABCDE_N-F and CsuABABCDE_S-R. The PCR product was digested with restriction enzymes *Not*I and *Sac*I and cloned in *Sac*I-*Not*I digested pBAD-ENSPA downstream the P_{BAD} promoter (1). The resulted plasmid was named as pBAD-Csu. Deletions of genes of the CsuA/B, CsuA, CsuB, and CsuE subunit in pBAD-ABABCDE were constructed by reverse PCR using oligonucleotides Δ -CsuAB-R and -F, Δ -CsuA-R and -F, Δ -CsuB-R and -F and Δ -CsuE-R and -F, respectively. Replacements of residues 40-43 (LALA) to SGSG (L₄₀ALA₄₃ \rightarrow SGSG), 140-145 (IVGIGV) to SSGSGS (I₁₄₀VGIGV₁₄₅ \rightarrow SSGSGS), 157-159 (LGI) to SGS (L₁₅₇GI₁₅₉ \rightarrow SGS) in CsuE were generated by reverse PCR and oligonucleotides CsuE-LALA_R and -_F, CsuE-IVGIGV_R and _F and CsuE-LGI_R, respectively. The L₄₀ALA₄₃ \rightarrow SG mutation was introduced by accident, as a side product of the PCR intended to introduce the L₄₀ALA₄₃ \rightarrow SGSG mutation.

To express isolated N-terminal domain of CsuE (CsuE_{NTD}), synthetic nucleotide sequence encoding the first 205 residues of CsuE including the secretion sequence peptide was ordered from GenScript and inserted downstream of the *T7* promoter in the pET101D expression vector (Invitrogen). To facilitate the purification of the domain a C-terminal His tag was added to the expression plasmid using reverted PCR and primers CsuEN6Hrev and CsuEN6Hfwd. To improve the protein stability and increase the level of expression, codons for Pro206 and Asp207 were introduced preceding the His tag coding region by reverse PCR using primers CsuE-N6H_PR and CsuE-N6H_DF. The resulting plasmid was termed pET101-CsuE-NPD6H.

To generate the $I_{140}VGIGV_{145}$ \rightarrow SSGSGS mutation in CsuE_{NTD} and CsuE co-expressed with CsuC, plasmids pET101-CsuE-NPD6H and pET101-CsuC6H-CsuE, respectively, were amplified using oligonucleotides CsuE-IVGIGV_R and CsuE-IVGIGV_F. The PCR products were blunt-end ligated, resulting in expression plasmids pET101-CsuE-NPD6H-SSGSGS and pET101-CsuC6H-CsuE-SSGSGS.

Analysis of CsuE binding to plastics. Wild type and $I_{140}VGIGV_{145} \rightarrow SSGSGS$ mutant CsuE complexed with the CsuC chaperone were purified essentially as described in (2). To enable detection of the protein by measuring time-resolved fluorescence, purified complexes were labeled with Eu⁺³-chelate. 65 μ M complex was incubated with 194 μ M Kajo615 Eu⁺³-chelate (Kaivogen) in 88.6 mM bicarbonate buffer, pH 9.8 at 4°C for 18 h. The reaction was stopped by adding 20 μ l 3.0 M Tris-HCl, pH 8.45. Labeled proteins were kept on ice until gel filtration on a Superdex75 10/300 GL column (GE Healthcare) equilibrated with 50 mM Tris-HCl (pH 7.5) and 150 mM NaCl (buffer A). Eluted proteins were concentrated on a Vivaspin device with 5 kDa molecular weight cut off (GE Healthcare). Protein concentration was measured using a NanoDrop 2000 spectrophotometer (Thermo Scientific).

To ensure the comparability of the wild type and mutant binding experiments, the two were measured simultaneously, side-by-side. Labeled complexes (60 µg/ml in buffer A) were first incubated on ice in a 2 ml polypropylene tube (Sarstedt) for 30 min to ensure that the concentration is no longer changed due to binding to the plastic tube. 1 ml of the wild type and mutant proteins were pipetted simultaneously onto two 5.5 cm Petri dishes (Sarstedt) and shaken horizontally by hand to ensure the volume covered the entire bottom surface of the dishes. The binding experiment was done at 22°C with 250 rpm shaking on an automatic shaker (New Brunswick Scientific) to maintain uniformity of the sample volume. 7.2 µl samples were withdrawn at different time points and added into wells of a SpectraPlateTM-96HB (PerkinElmer) plate for measuring Eu^{+3} fluorescence. To estimate the initial concentration of the complex (0 time point of the reaction), 7.2 µl of the protein was taken for the fluorescence measurement directly from the tube. The samples were mixed for 10 to 15 min with 140 µl of Europium Fluorescence Intensifier (Kaivogen). As the fluorescence signal was very high, each sample was divided after mixing into three wells and the sum of signals from the three wells was used as the signal value. The delayed fluorescence was measured using a Victor3 1420 multi-label counter (PerkinElmer). The binding curves were corrected for evaporation from the plate. The evaporation effect was estimated by measuring the change in fluorescence of an unreactive form of the Kajo615 label incubated on a Petri dish in 1 ml buffer A, containing 1.94 pM BSA.





Csu pili mediate biofilm formation of recombinant *Escherichia coli* on abiotic surfaces. Csu pili expression was induced (+) or not induced (-) in *E. coli* harboring pBAD-Csu and pYFP plasmids. Bacterial cells were incubated in polystyrene (A and B) and polypropylene (C) tubes for 6 h at 37° C in LB medium. Attached cells were detected by staining with crystal violet (A) or by observation of fluorescence owing to the expression of yellow fluorescence protein (B and C). To study binding to the hydrophilic surface of cellophane (D), straps of cellophane were added to the tubes and incubated with bacteria expressing or not expressing Csu pili, gently washed and analyzed as in (B) or (C). Although biofilm was observed on hydrophilic cellophane (D), cells were detached from these surfaces much more easily than from hydrophobic polystyrene, polypropylene or polyethylene surfaces.





Representative transmission electron microscopy micrographs of *E. coli* **expressing Csu pili.** *E. coli* strain BL21 harboring the pBAD-ABABCDE plasmid was cultured in LB medium in presence (**A**, **C** and **D**) or absence (**B**) of arabinose and stained with ammonium molybdate. Micrographs of different magnification are shown. The arrow in **A** indicates an individual pilus clearly seen on the image. The Csu pilus is about 3.5 nm in diameter and is typically 1-2 μ m long. However, some pili can reach 5 μ m in length (3-6 times longer than the prototypical classical type 1 and P pili) and form long bundles well visible in (**D**).





Effect of mutations on Csu pilus expression. *E. coli* harboring pBAD-ABABCDE derivatives, carrying deletions of entire genes of CsuA/B (A), CsuA (B), CsuB (C and D), CsuE (E) or a substitution of residues 140-145 in CsuE with SSGSGS (I_{140} VGIGV₁₄₅ \rightarrow SSGSGS, F), were cultured in LB medium in the presence of arabinose and stained with ammonium molybdate. Deletion of genes coding for CsuA/B and CsuE completely abolished the pilus assembly. Δ CsuA and Δ CsuB mutants expressed a few thick and long pili (B-D). The I_{140} VGIGV₁₄₅ \rightarrow SSGSGS mutation did not affect pilus assembly (F).



Quantification of biofilms of *E. coli* harboring the wild type and subunit deleted *Csu* gene cluster. An entire gene of CsuA/B, CsuA, CsuB or CsuE subunit was deleted (Δ) from the *Csu* gene cluster. Arabinose was added to induce pilus expression. Uninduced wild type (WT) cells were used as a negative control. Biofilms were stained with crystal violet, processed as described in Materials and Methods, and quantified by measuring absorbance at 595 nm.



Structural comparison of two copies of CsuC-CsuE in the asymmetric unit. Molecules were superimposed by distance minimization between C α atoms of CsuC. CsuC and CsuE are colored red and green in one complex and magenta and marine in another complex, respectively. Note that major differences are observed in the region of the N-terminal domain of CsuE. Most of these differences are caused by a change in the angle between domains in CsuE.



Fig. S6

The angle between N- and C-terminal domains in CsuE is sharper than that in two-domain adhesin subunits from the classical (FimH) and alternative (CfaE) CU systems. CsuE (cyan), FimH (yellow), and CfaE (magenta) were superimposed by minimizing distances between C α atoms in β -strands of their C-terminal, adaptor (pilin) domains. Stereo pairs of C α -traces are shown. The angles between domains in CsuE, FimH, and CfaE are ~135°, 150°, and 180°, respectively, as measured from the center of gravity of each domain to that of the connector. The shape of CsuE is closer to that of the FimH adhesin from classical type 1 pili. The angle between domains in FimH (~150°) has been suggested to be a part of mechanism for shear-force-enhanced attachment to receptors (5).





*Total residues of protein shown in the column

Structural comparison of C- and N-terminal domains of CsuE between each other and the major CsuA/B pilus subunit of Csu pili. (A and B) Cartoon diagrams of superpositions (stereo views) of C- (magenta) and N-terminal (cyan) domains of CsuE (A) and C-terminal domain of CsuE (magenta) and CsuA/B (green) (B). Disulfide bonds are shown as stick models. Secondary structure elements in the C-terminal domain of CsuE are labeled. CsuEpd and CsuA/B have a very different structure of β -sheet 1, ABED (**B**). In CsuA/B, β -sheet 1 is split in the middle due to the loop insertions that interrupt its β -strands as in most CU subunits (6). In contrast, β -sheet 1 in CsuEpd is uninterrupted, making the structure of CsuEpd more similar to the canonical Ig-like fold of the 8-stranded h-type (7). Consistent with the h-type fold, strand D switches sheets, but then repeats this twice. CsuE_{NTD} and CsuEpd share a highly conserved disulfide bond connecting strands A and B (Fig. S11), but the structures of these domains differ substantially, and CsuE_{NTD} is structurally distant from major pilin CsuA/B. (C) Structural comparison statistics. Superpositions and statistics were generated with the DaliLite server (http://ekhidna.biocenter.helsinki.fi/dali lite/start) (8).



Structure of the CsuC-CsuE complex highlights the characteristic features of non-classical assembly. (A) Chaperone-bound pilin domain (CsuEpd) has a large fraction of disordered or poorly ordered sequence. Close-up of the CsuC-CsuE structure, showing the structure of CsuEpd (cartoon diagram, stereo view). CsuE is colored by B-factor of Ca atoms with the color ranging from blue to red and corresponds to a B-factor range from 20 to 135 Å². CsuC is shown in magenta except for β-strand G1, which is violet. Donor strand residues are shown as sticks. Note the missing loops and elevated B-factors in the structure of CsuEpd distant from CsuC. (B) CsuC uses both domains to anchor the C-terminal carboxylate of CsuE rather than one as in the classical chaperones. Close-up of the CsuC-CsuA/B structure, demonstrating interactions between C-terminal carboxylate of CsuE and CsuC (cartoon diagram). The complex is painted as in Fig. 2. C-terminal Phe312 in CsuE and Tyr9, Arg89, Tyr196, and Arg174 in CsuC are shown as ball-and-stick. Hydrogen bonds are shown with dashes and their length is indicated. Residues Tvr9 and Arg89 belong to domain 1, whereas residues Tvr196 and Arg174 belong to domain 2. Tyr9 binds to the carboxylate via a structured water molecule (red sphere). This previously unidentified contact is also present in the CsuC-CsuA/B complex (6). (C) The donor strand motif in CsuC in the CsuC-CsuE complex is shifted towards the end of the G₁ strand relative to that in classical chaperones. Fragment of the superposition of CsuC-CsuE and Caf1M-Caf1 complexes, showing the alignment of G₁ donor strands in CsuC and Caf1M. Hydrophobic donor residues are shown as ball-and-stick and labeled. Positions of hydrophobic pockets P0-P5 in subunit acceptor clefts (P0-P3 in CsuE and P1-P5 in Caf1) are shown schematically above the donor strands.





Cartoon diagram of CsuE illustrating the interface between N- and C-terminal domains (stereo view). N- and C-terminal domains are painted in blue and cyan, respectively. Residues engaged in interdomain contacts are shown as sticks. A structured water molecule participating in a network of hydrogen bonds between the two domains is shown as a red sphere. Hydrogen and ionic bonds are shown as dashed lines; the bond length is indicated. β -Strands and C-terminus are labeled. The buried area in Csu (383 Å²) is only half of that in the CfaE subunit of CFA/I pili assembled via the alternative CU pathway, despite a similar size of the linker (9). This is explained by the striking difference in the angle between domains in these molecules (Fig. S6).



D

Z-score; RMSD (Å); superimposed residues/total residues*					
	CsuE N-domain	CfaE N-domain	FimH N-domain		
CsuE N-domain		6.9; 3.2; 114/179	5.5; 3.7; 116/179		
CfaE N-domain	6.9; 3.2; 114/178		4.5; 3.4; 98/178		
FimH N-domain	5.5; 3.7; 116/158	4.5; 3.3; 98/158			

*Total residues of protein shown in the column

Structural comparison of N-terminal domains of CsuE, CfaE, and FimH. (A and B) Cartoon diagrams of superpositions (stereo views) of N-terminal domains of CsuE (cyan) and CfaE (pink) (A) and CsuE (cyan) and FimH (green) (B). Binding fingers 1-3 in CsuE are painted in yellow, orange, and light orange, respectively. Secondary structure elements in CsuE are labeled. Conserved disulfide bonds are shown as stick models. (C) Topology diagrams of CsuE, CfaE, and FimH. Strands and helices are shown as arrows and cylinders, respectively. (D) Structural comparison statistics.

Fig. S11

	A1	A1'	<i>α1</i>	B11	B12		C1	1 C12	(C11/D1
	-									
	^	10	20	30	,	40	50	60	1	70
PAM18_4750/1-291	ACTTS	SG T <mark>G N F G S</mark> L S	<mark>S</mark> F T <mark>V</mark> A S T A -	- QT I TGT T	GFK <mark>C</mark> TG	SLL SILSTNT	I DAT I	ASTANPLGTTPRL -	Y NAA S <mark>G</mark> TYL	PYSICKDNGC
Q7S_18315/1-296	GCTTA	PGSITLGTQN	S FAVSSSP -	- LITSGGS	GLSCTG	GLL NIAGTNT	TAFI	GVTQHPSNSQPRL -	Y SGT TGQYL	PYSLCKDASC
SOD c19210/1-288	DCATT	NGSVTLPGGS	S FTVYNGQ -	- I SAQGTA	GLNCTG	LGL SLLSQNT	VTVKI	TSTTHNMAI A -	N T DG SG DQ I	PYLIYPDSNY
YP_1720/1-292	<mark>C</mark> TF S	SPTVT <mark>L PP</mark> NS	S FNVNTLT -	- E S G S G T I	AML CTG	T <mark>GV</mark> SLLASPV	LNATV	ASTTNTLKL K -	N S A <mark>G</mark> DV I	I P Y T I Y SDAGY
PP1Y_Mpl9692/1-301	ACSAT	SGSVNLGSAS	S FTVASAA -	- QRAGGAT	GFSCTG	SLL SIVSTNT	ITATI	ASATNSQGTQPRL -	R DAT T <mark>G</mark> DS I	RYDICKDSSC
Entas_2592/1-302	ACTIS	SVNASL GTVT	S FSLSGIGE	- VEIIGIL	TVNCCS	- AV - LNLLINDS	VILSY	I SASVSGNSRAIMK	R I DNA I I I DV I	P RL CGL SGC
PP4 34580/1-300	KCTSVAT-	- SAAAFGSLN	S - TOVRTTVO	- TASSANS	GLQCNG	SVL - SVLSSTDS	EVVKI	G-LV	GP T <mark>G</mark> DV	PYTLYADATT
YE1856/1-302	DS <mark>CTF</mark> S	PGTVTLPPSS	<mark>S</mark> - - V T <mark>A</mark> G T T A -	- VNAQ <mark>G</mark> AT	AMT CPG	ALISITLLGSFT	SATI	SGTTNNLNL K -	N E V <mark>G</mark> DL I	I P Y S I Y RTGTF
Pput_3332/1-301	LCSSVAT -	- LPAAFGSLN	S TQVRNTVQ	- TASSLNS	GLQCTG	SLL - TVLSSGDH	FYAT I	G-LV	GPTGDV	PYTLYADNTT
H045 11630/1-304	ACSVAAS-	- VPASEGSIS	S MTVRTAAQ	- ASSTTSA	GLSCTS	ALI-SLLVPSDH	YATI	G-LV	GP TGDV	GYTIYGTNTA
M634_16975/1-302	<mark>C</mark> E I TAL -	TPSIQFGSVS	S F T V S S T Q Q	QSSAQPHA	GITCDF	STL - VSLLSGDY	SVTF	T S L NG G Q M T	T QGD ASS I	NYQIFGDSSL
PFL_3949/1-304	LCTTVPT-	- APAGFGTVS	S I L V R T T S Q	- PASTTNA	GLSCTG	SLL - SILASNDH	YATI	G-MV	GP T <mark>G</mark> DV I	SYTLYANNST
PAGR_g0744/1-305	ACIL P	ASSASEGIQI SSTASEGIVS	I FVANISV -	- STISINA		GIA-LILLSNNQ	IFQL	I SASNINGIRGILK	R SGDT - GSDN T VST - GTDN	PURECIDSAC
ESA 01347/1-298	DCRVS	GTGAAYGSQT	SFVINSTV-	-QTTTATL	TLDCD-	- SV - LNVLNNDF	VTLTL	TGATTTAGTRATLG	R SGD TTDR	PVQVCAQSGC
ROD_19341/1-301	A <mark>C</mark> RVS	TTN <mark>GAFGSV</mark> S	<mark>S</mark> F T V N S T E -	- Q S T S A S L	VVQCD-	- VV - LGLLNNDT	ITLTY	TGATVSASNRATLK	R SDNATVTDV	PV RMCAQSAC
ECENHK_13825/1-302	ACTIS	TVNASFGSVT	S FAL SGTGE	- VETTGTL	VVACD-	- AV - LNVLTNDS	VTLNY	TAASVSGNSRANLK	R TDDTSITDV	PTRLCGLSGC
ACaV_4532/1-291 BMASAVP1 A1401/1-294		AAASEGTVT	S QRVL SGPA	- STSTTSS	GLSCSG	ALL - GLEVIGDO	INASI	G-LI		PYQTINLAGA
BPC006_11682/1-294	TCSVVSA-	- AAASFGTVT	S FAVARQPO	- STSTTSS	GLSCSG	ALL - GLFVIGDQ	INASI	GKLV	GP TGDA	PYTVFADQNY
MDS_2712/1-298	<mark>C</mark> STY	TASAN <mark>LGST</mark> N	<mark>S</mark> L T L R T S Q -	- Q S T A A <mark>G</mark> A	GL S <mark>C</mark> PG	VLQAL TSAY	VRVTL	Q N T G S L V -	L S D G K <mark>G</mark> N Q I	I P F Q V Y R D A G Y
YPC_2125/1-292	CTFS	SPTVTL PPNS	S FNVNTLT -	- ESGSGTI	AML CTG	TGV SLLASPVL		K-		PYTIYSDAGY
ECA3077/1-297	ACTTP	PSNTVLGPYG	SVVGVNGTP -	-QVVASGS	GFRCTG	SVL SLASTNT	TATI	QSDSNPSGTTMRM-	R RGT TTDY	PYSLCMDSGC
NCGM2_0934/1-291	ACTTS	SGT <mark>GNF</mark> GSLS	<mark>S</mark> F T V A S T A -	- Q T I TGT T	<mark>GFК</mark> СТG	SLL SILSTNT	I DAT I	ASTANPLGTTPRL -	Y NAA S <mark>G</mark> T Y L	PYSICKDNGC
CsuE/1-312	ACSVSAS-	GTS <mark>S</mark> ISVP	S - IYLMENGE -	- NSSQFNS	GLSCTG	FSL ALANMTYL	LKYRV	EQMSNSFTN	AQ TGEKL	NAIILDS
BJAB0868_02454/1-312 A3UG_03070/1-299	ACSVSAS-	PAAINEGSVV	A GNAA	- NSSQENS	KESCOA	DNN GTIF Y		SSMD APPEOM	ISTGDOFGKOYS	LERLENGVAH
P795_6510/1-297	ACTVSGTT	NSTENYTAAN	I NSDATV	NL SG	TITCTN	ILGL PQ I SI	NFMCM	KTVFTGA TT	ANNSVT	PYTVTATVGG
PSYCG_09745/1-300	IGSGPIACTQVGST	INDLNFGTVN	P F S S T T -	S T S A T I	NYECRG	SE <mark>G</mark> RA ST /	ARICY	TFGPLNT DDH	KLLG PNNTTL	AFDLFSSSSH
XCC1378/1-316	DTNCTVTL	GTPLAFGNVA	A NG T T	DAVATL	NVSCAT	AAL SVLGYAH	SLCL	DLGPGSASAG - LYAPRRM	L N PTSDSL	DEQLYSEATR
VAPA_1c20560/1-308	AVSCNAT-	MTALNEGTVE	L VDGSTP	- PSVNATL	TYTCNN	ITGN S TESL		NIGDGDQSLG - SFDPRLM	K - L T TGNNTL	KFRLFQGTSG
Sinme_6943/1-295	QS <mark>C</mark> NFS-	ISNLNFGAVD	т <mark>L</mark> S <mark>G S</mark> Q T	N S T A T I	NINCTG	L T L Q R I	I L I <mark>C</mark> P	NLGAGSGGSS - SAAA <mark>R</mark> QM	L NG A NL <mark>L</mark>	NYQLYSDSAR
Bcep18194_A5756/1-299	DACSVT-	PPAPSEGSVSI	P I RLLAV	TTTSTM	TVNCTW	DVL SL NTG		NLGG TSPRYL	S NGT NQ	QYDLYQDSGY
BBK 506/1-295	FTCSVT-	TPAPNEGSVD		STTATE	TVTCTW	/SAL TL TPN			T NGS ERL	OYDI YODSGH
Rta_34890/1-282	AISCSLS-	SSGFTTVY	S EN I TAA	- NSTVGTV	TLTCTR	SNLAD - DPTVFN	SLRA	DDGQQASNGIN RARLN	N SNGNGSSNF	GYDLWRDPAC
BYI23_D012110/1-291	QT CTF S -	VGYTNFGTIS	A I RTEPE	DIV <mark>GG</mark> I	HIL CSG	YTT PM	V RM <mark>C</mark> L	NISA TAP <mark>R</mark> QL	L G P D <mark>G</mark> A A L	NYNLYVDPDH
ABO_0699/1-294 BPPE64_DCDS03180/1-30	DN	SPTLDFGATD	P FMAGPL	NANTQI	QWSCSR	GIGVLESIPI	FKMCI	YVAADNDGG ILPRNL	RPA NP <mark>G</mark> PA	PENVYTLLVG
AXYL_05495/1-300	QTCTVS-	MAPITFPNLN	P VLGSSV	TQTGTL	SVTCTW	/GLL TG GY - /	ARVCV	SLGIGSGS - T - VQDPRQM	A NGANR	QYRLAPSSSM
Smlt1510/1-323	VAV <mark>C</mark> AA VA	DPTL PFGNVN	s N А <mark>Р G</mark> А Т	T <mark>G</mark> TLNI	т <mark>үтс</mark> тт	AAL SLLATTG	v r v <mark>c</mark> v	GIGAGSGGGS-SSSW <mark>R</mark> TM	к т SASDS <mark>N</mark>	INFQLYNTSNF
OA238_c46250/1-288	ALVCETN	IVSLDFGTIS	V RDGLPQ	QT SGPV	TISCFG	GTP GTT		TLGSGSGGAAAGQSPRYL	T R AGSATL	QYQL SSQNSF
XOO1979/1-316	DTTCTVTL	GTPLAFGNVA	V NG T T	DAVATL	NVSCAT	AAL SVLGYAQ	VSLCL	DLGPGSASSG - I YAPRRM	L N ST S D G L	DFQIYSEATR
	*	•			*		:	1		•
	D									
	D1			α2		E11	E12		F11	F12
	D1	•		α2		E11	E12		F11	F12
	D1	•		α2		E11	E12		F11	F12
	80 80		90	α2	100	E11	E12	110	F11	F12
PAM18_4750/1-291 Q75_18315/1-296	80 GT VYNVGSTVF SA VYNGGT I S		90 F		100 NAT	E11	E12	110 TAT GVTL P	F11	F12 130 GLNWAWH-
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297	80 GT VYNVGSTVF SA VYNQGDT IS SP AYQDGGV IS	- WSSTT - WSSTT - WSRTT	90 	α2 LGILGLF LGLLGLF LELLGLF	100 NAT SGP NSG	E11 DGSL NSTL DGTM	E12 PLYL PLYV PLYF	110 TATGVTLP PVASSNLA TTPGANVP	<i>F</i> 11 * * * AGTYTDTI AGTYTDVI AGTYTDVI AGTYTDVL	F12 130 GL NWAWH - P I SWTWN - T I TWV YR -
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_c19210/1-288	80 GT VYNVGSTVF SA VYNQGTI IS SP AYQDGGV IS QY AYSVGQTI IS	- WSSTT WSSTT WSRTT YSSL	90 	α2 LGILGLF LGLLGLF LLSLILI	100 NAT SGP NSG ISS	E11 DGSL NSTL DGTM NVNF	E12 PLYL PLYL PLYV PLYF PMYV	110 TAT GVTL P PVA SSNL A TTP GANVP TTA GANVR	<i>F</i> 11 AGTYT DTI AGTYTDVI AGTYTDVL SGTYTDVV	F12 130 GL NWAWH P I SWTWN T I TWV YR NL TWN YH-
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_c19210/1-288 YP_1720/1-292 P91Y_M01982/1.301	80 GT VYNVGSTVF SA VYNVGSTVF SP AYQDGGVIS QY AYSVGQTIE NN AIAIGNVIN TA TVAVGSTI	- WSSTT - WSSTT - WSRTT - YSSL - YAGNS	90 	C2 LGILGLF LGLLGLF LELLGLF LLSILI LLIVTLF	100 NAT SGP NSG ISS QI	E11 DG SL NSTL DG TM NVNF SANL GG TU	E12 PLYL PLYV PLYF PMYV PIYI	110 TATGVTL P	F11 	F12 130 GLNWAWH- PISWTWN- TITWVYR- NLTWNYH- NLNWNYD- SIDWTWH-
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_e1921011-288 YP_17Z0/1-292 PP1Y_MpJ9692/1-301 Entas_2592/1-302	80 GT VYNVGSTVF SA VYNVGSTVF SP AYQDGGVIS QY AYSVGQTI NN AIAIGNVIN TA TYAVGSTI ASNSEVQISKTY	- WSSTT -WSSTT -WSRTT -YSSL -YAGNS - WSSTT - WSGN	90 	C - LGILGLF - LGLLGLF - LELLGLF - LLIVTLF - LGILGLF - LGILGLF	100 NAT SGP NSG ISS QI NAT GSK	E11 	E12 PLYL PLYL PLYF PNYV PIYI PIYI PIYI	110 TAT GVTL P PVA SSNL A TTP GANVP TGSNNA I NVNVS TGSNNA I NVNVS	F11 	F12 130 GLNWAWH- PISWTWN- -TIIWVYR- -NLTWNYH- NLNWNYD SIDWTWH- TFSINYN-
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_c19210/1-288 YP_1720/1-292 PP1Y_Mp16692/1-301 Entas_2592/1-302 ETA_04540/1-307	B0 GT VYNVGSTVF SA VYNVGSTVF SP - AYODGGVIS QY - AYSVGQTIS NN - A I AIGNVIN TA - TYAVGSTII ASNSEVQISKTYI ST - ELTIGGTAT	- WSSTT WSSTT YSSL YSSL WSST WSST TYSQSQ	90 	α2 LGLGLF LGLGLF LELLGLF LLSLILI LLIVTLF LGILGLF TLIGL TLIGL	100 NAT SGP ISS QI NAT GSK	E11 - DG SL - NSTL - OGTM - NVNF - SANL - GGTL - GTL - GYNI - VYP	E12 PLYL PLYV PLYV PLYF PIYI PLYF PLYF	110 TAT GVT L P TVA SSNLA TTA GANVP TGSNNA INNVS TGSNNA INNVS	F11 **** AGTYTDVI	F12 130 GLNWAWH- PISWTWN- TITWVYR- NLTWNYH- TFSINYN- SVLFTYR-
PAM18_4750/1-291 Q75_18315/1-296 K0X_23800/1-297 SOD_c19210/1-292 P17_Mp852/1-301 Entas_2592/1-302 Enta_5292/1-302 Enta_45801/-307 PP4_345801/-307	80 GT VYNVGSTVF SA VYNQGDTIS SP AYDGGVIS QY AYSVGGTI NN AI AIGNVI NN AI AIGNVI TA TYAVGSTII ASNSEVQISKTYI ST ELI IGGTAI TY PIITRGTGFF	- WSSTT	90 	α2 LGILGLF LGLLGLF LLSILL LLSILL LLSILL TLGLLGL TLGLLGL TNLANLL LDLGLLG	100 NAT SGP NSG QI NAT GSK GGF	E11 - DG SL - NSTL - DG TM - NVNF - SANL - GG TL - Q'NI - VFPI - TPKAV	E12 PLYL PLYL PLYV PLYF PLYF PLYF PLYF	110 110 114 T	F11 	F12 130 - GLNWAWH - - PISWTWN - - TITWVYR - - NLTWNYH - - NLTWNYH - - SULFTYR - - SVLFTYR - - NVEWTWK -
PAM18_4750/1-291 QTS_18315/1-296 KOX_23000/1-297 SOD_c19210/1-288 YP_1720/1-282 P1Y_Mple52/1-301 Entas_2592/1-302 ETA_04540/1-307 PP4_34500/1-300 YE1856/1-302 P014_33271-301	80 GT VYNVGSTVF SA VYNQGDTIS SP AYQQGGVIS GY AYSVGGTI NN AIAIGNVI NA TAVXGSTI ASNSEVQISKTYJ ST ELTIGGTAT TY PITRGTGFF SP ALPIGGKAT RY PITRGVAYT		90 	α2 LGILGLF LGLLGLF LLSLLGLF LLSLLLGLF LLSLLGLF TLGLLGLF TLGLLGL TLLGLL LDLLGLLGL	100 NAT SGP ISS QI QI GSK GGF SG GGT	E11 -DG5L -NSTL -DGTM -NNF -SANL -GGTL -GYN -VFPI -TPKAV -NANL -TPKAV	E12 PLYL PLYL PLYF PLYF PLYF PLYF PLYF PLYF	110 TATGVTL P	F11 	F12 130 - GLNWAWH- - PISWTWN- - TITWVYR- - NLTWWYD- - NLTWWYD- - SIDWTWH- - TSINYN- - SVLFTYR- - NVEWTWK- - NLEWWW- - TVAWWYD-
PAM18_475011-291 Q75_1831511-296 KOX_238001-297 SOD_c192101-288 VP_17201-282 PP1Y_MpJ69221-301 ETA_045401-307 PP4_3458011-300 YE158561-302 Pput_33321-301	80 GT VYNVGSTVF SA - VYNQGDT IS SP - AYSUGGT IE QY - AYSUGGT IE QY - AYSUGGT IE TA - TYAVGST I TA - TYAVGST I TA - TYAVGST I ST - ELT IGGTAL TY - PI TRGVAFI RY - PI TRGVAFI RY - PI TRGVAFI SY - PI TRGVAFI	L.WSSTT WSSTT YSSL YSSL WSGN TYSOSQ FRTTG FRTG FARNG FARNG	90 F A N N S F F I S I I	C2 -LGILGLF -LELGF -LELGF -LLSLILF -LLIVTLF -LGILGF -TLGLGL -TLLGLGL -TLSISL -LLSISLG -LLSISLG -LLSISLG -LLSISLG -LLSISLG	100 NAT	E11 DGTM NSTL DGTM NNNF SANL GGTL QYNI VFPI TPKAV NANL TFKAV SRTV	E12 PLYL PLYL PLYF PIYI PIYI PIYI PIYI PIYM PIYI PIYM PIYI	110 T AT GVT L P PVA SSNLA TTP GANVR TGA	F11 	F12 130 - GL NWAWH- - P I SWTWN - TI TWVYR - NL TWWYH - NL NWYH - SI DWTWH - SI DWTWH - SV EVTWK - NV EWTWK - NU AWNYN - TV AWSWD - TN AWSWN
PAM18_4750/1-291 QTS_15315/1-296 (KO_23800/1-297 SOD_c19210/1-288 VP_1720/1-282 PPTY_M0J6920/1-301 Entas_2592/1-302 Enta_4580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_5EEM3394/1-301 H045_11630/1-304	80 GT VYNVGSTVF SA VYNQGDT IS SP AYQGGT IS GY AYSVGGT IC NN A I . A IGNVI NN A I . A IGNVI TA TYAVGST IT ASNSEVQ ISKTYT ST ELT IGGTAT TY P I TRGTPFI SP A LP IGGKLT RY P I TRGVPFI SY P I SRGVPFI SF - P I ARNOF	L WSSTT	90 F - A A - A S - F F	C2 - LGILGLF - LGLLGLF - LELGF - LLSLILI - LLSLILI - TLLGL - TLLGL - TLLGL - LDLGL -	100 NAT SGP NSG ISS QI NAT GGF NG SL GGF NGS IAGP	E11 DGSL NSTL OGTM NVNF SANL GGTL QYNI TPKAV TPKAV SPKTV GTKT	E12 PLYL PLYL PLYV PIYI PIYI PIYI PIYI PIYI PIYI PIYI PI	10 TATGVTLP PVASSNLA TATGANVP TGS.NNAINVNVS TGS.NNAINVNVS TGAGOVA TVAGANVP TIAGANVP TGS.NNAINVNVS TGAGNVA TVAGANVP TLPNAVVP TLINAVVA TGNNOVISTNIS TOIGSNVA TVYGANVA SITGANVA	F-11 	F12 130 - GL NWAWH- - PI SWTWN- - NL SWTWH- - NL TWNYH- - SUL TYR- - NL AWYN- - NL AWYN- - NL AWYN- - NL AWYN- - NL AWYN- - NL AWYN- - NL AWYN-
PAM18_4750/1-291 Q75_18315/1-296 (KOX_23000/1-297 SOD_c19210/1-288 YP_1720/1-202 P1Y_Mp18692/1-301 Entas_2592/1-302 ETA_04540/1-307 PP4_34580/1-302 Pput_3332/1-301 P9EEI3334/1-301 P9EEI3334/1-301 P9EEF334/1-304	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYOGGVIS QY AYSVGGTII NN - AIAIGNVI TA TYAVGSTII ASNSEVQISKTYJ ST ELTIGGTAI TY PITRGTGFF SP ALPIGGKLI SY PISRGVGFF SF PISRGVGFF SF FIYFRGVGFF SF FIYFRGVGFF	L WS STT	80 F A A N S F F C C C C C C C C C C C C C C C C C	C2 LGILGLF LGLLGLF LLSLLGLF LLSLLGLF LLSLLGLF TLLGL TLLGL TLLGL LLSISLG LDLGL LDLGLG LDLGLG LDLGLG	100 NAT	E11 DG SL NSTL DG TM NVNF SANL GG TL Q'NI TPKAV NANL TPKAV SFKTV GTKTV VEF TVAV	E12 PLYL PLYL PLYF PLYF PLYF PLYF PLYF PLYL PLYL PLYL PLYL PLYL	110 TAT	F-11 	F12 GL NW&WH- PI SWTWN- TI TWVYR- NL TWWYH- NL TWWYH- SI DWTWH- TSI NYN- SI DWTWH- TSI NYN- NL AWWYN- NL AWWYN- NL AWWN- NL AWWN- NL AWWN- NL AWWN- NL AWWN- NL AWWN- NL AWWN- NL AWWN- NL AWWN- NL AWWN-
PAM18_4750/1-291 QTS_18315/1-296 KOX_2300/1-297 SOD_c19210/1-288 YP_1720/1-282 PP17_Mpl952/1-301 Entas_2592/1-302 PP14_34580/1-300 YE1556/1-302 PP4_3352/1-301 P945_3324/1-301 H045_115301-304 M634_16975/1-302 PFL_3349/1-304	80 GT VYNVGSTVF SA VYNQGDTIS SP AYQGGVIS QY AYSVGJTIF NN - A IAIGNVIN TA TAVKSTI ASNSEVGISKTYJ ST ELTIGGTAI TY PITRGVATI SY PISRGVGFT SF PIARNTOFT SF PIARNTOFT	L-WSSTT	80 F A V V S F F V V V V V V V V V V V V V V V	C2 -LGLGLF -LGLLGLF -LGLLGLF -LLSLLGLF -LLSLLGLF -LLSLLGLF -LGLGLF -LGLGLF -TLLGL -LDLGL -LDLGL -LDLGL -LDLGLF -LDLGLF -LDLGLF -LDLGLF -LDLGLF -LDLGLF -LDLGLF	100 NAT	E11 - DG5L - NSTL - DGTM - NNNF - SANL - GGTL - GYNI - VFP - TYAKT - VEF - TYAKT - VEF - TYAKT - VEF	E12 PLYL PLYL PLYV PLYF PLYF PLYF PLYF PLYF PLYF PLYL P	110 TAT GVT L P PVA SSNLA TTP GANVP TTA GANVR TGA GTOVA TVA	F11 	F12 130 - GL NWAWH- - P I SWTWN - - T I TWVYR - - NL TWWYH - NL NWYH - SI DYTWH - TS I NYN - SV EVTWK - NL AWWYN - NL AWWYN - NI AWSWN -
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_c19210/1-288 VP_1720/1-282 PP1Y_MpJ6922/1-301 ETA_04540/1-307 PP4_34580/1-300 VE15856/1-302 Ppu1_3332/1-301 H045_11530/1-304 M634_169771-302 PFL_3349/1-304 PFL_3494/1-305 EbC_38210/1-306	80 GT VYNVGSTVF SA - VYNQGDT IS SP - AYSVGGT IG QY - AYSVGGT IG QY - AYSVGGT IG TA - TYAVGST I TA - TYAVGST I TA - TYAVGST I ST EL TIGGTAF SF - ALP IGKLI RY - PI TRGVAFI SF - ALP IGKLI SF - PI ARNTOFI SF -	1- WSSTT WSSTT YSSL YSSL WSSTT WSST WSST F RTTG F RTTG F ARNG F ARNG F ARNG F ARNS V YNSAT N YSQAQ	80 F A N S F F F I I I I I I I L L L	02 	100 NAT	E11 - 065 L - NST L - 06T M - NNNF - SANL - 66T L - 67 N - 77 N - 77 NA -	E12 PLYL PLYL PLYV PLYF PLYF PLYF PLYF PLYF PLYF PLYF PLYL PLYL PLYL PLYL PLYL	110 TAT	F11 	F12 130 - GLNWAWH- - PISWTWN - TITWVYR - NLTWWYH - NLWWYH - SIDWTWH- - SIDWTWH- - SVEWTWK - NLAWWYN - NIAWWN - NIAWN - NIAWWN - NIAWWN - NIAWWN - NIAWN - NI
PAM18_4750/1-291 QTS_15315/1-296 (KOX_2300/1-297 SOD_c19210/1-288 VP_1720/1-282 PP1Y_M0J692/1-301 Entas_2592/1-302 Entas_4580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_3491/1-304 PAGR_0074/1-305 ESA_01347/1-288 ROD_193/41/1-304	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYSUGGVIS QY - AYSUGGVIS QY - AYSUGGVIS GY - AYSUGGVIS ST ELIGGTAI TY - PITRGYAFI SF ALPIGGKLI RY PITRGYAFI SF PIARNTOFI SF PIARNTOFI SF PIARNTOFI SF PIARNTOFI SF PIARNTOFI ST EITIGGSAT AN ELIGGSAT ASNNFIAGGSYT	- WSSTT WSRTT YSSL YSSL YSSS FARGS FARGS FARGS FARG FARGS FARS YNSSAT YSGAQ WTGQ	90 F	02 	100 NAT	E11 -DGSL -NSTL -OGTM -OGTM -NVNF -SANL -GGTL -QYNI -VFPI -TPKAV -VEP -TVKTV -VEF -TVKTV -VEF -TVKTV -VEF -TVKTV -VEF 	E12 PLYL PLYL PLYV PLYF PLYF PLYF PLYF PLYF PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYF P	10 TATGVTLP PVASSNLA TATGANVP TGS.NAI.NVNVS TGS.NAI.NVNVS TGS.NAI.NVNVS TGAGANVP TTAGANVP TGS.NAI.NVNVS TGAGANVA TVAGANVA TVAGANVA TLINANVA TGN.OVISTNIS TVYGANVA SITSNVA TLTSSNVA TVAGGTVA TVPGGTVA TQ TQ	F-11 	F12 100 - GL NWAWH- - PI SWTWN- - NL TWNYH- - NL TWNYH- - SL DWTWH- - TS I MYN- - SS LI FTYR- - NU AWYNN- - NL AWWYN- - NL WWYN- - NL WWYN- - NL WWYN- - NL WWYN- - NL WWWN- - NL WWYN- - NL WYN- -
PAM18_4750/1-291 Q75_18315/1-296 (KXQ_23000/1-297 SOD_c19210/1-288 PP1Y_Mp18692/1-301 Entas_2592/1-302 ETA_04540/1-307 PP4_34580/1-302 Ppu1_3332/1-301 P945_13334/1-301 P945_13334/1-301 P945_13334/1-301 P455_1302 Pp1_34975/1-304 PAGR_00744/1-305 EbC_38210/1-306 EbS_01347/1-288 ROD_13941/1-301 ECENHK_1325471-302	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYOGOGVIS GY AYSVGGTII NN - AIAIGNVI TA TYAVGSTII ASNSEVQISKTYI ST ELTIGGTAI TY PITRGTGFE SP ALPIGGKLI SY PISRGVGFT SF FINGVGFT AN ELTIGGSAF AT EIAVGGYTI PSGSELAINGSYF ASNSEVQISKSYI	L WSSTT WSSTT WSRTT YSL YSSL RSTT WSSN FRTIG FARNG FARNG FGTGGG FGTGGG FARNS YNSAT NYSAA WTSQ WSSN	80 F - A - L - A - N - S F - F 	02 	100 NAT	E11 - DG SL - NSTL - DG TM - NVNF - SANL - GGTL - O'NI - VFP - TPKAV - NANL - TPKAV - SPKTV - VEF - TVAKTV - NFSI - RYTF - RFTL - RYNI	E12 PLYL PLYL PLYV PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL	110 TATGVÍLP PVASSNLA TTPGANVP TTGSNNAINVNVS TGSNNAINVNVS TGAGTQVA TVAGANVR TGNNGVISTNIS TGISNVA TVAGSNVA TVYGANVR TSSNVA TQISNVA TVYGANVA TSITSSNVA TVAGOTVA TVPGOTVA TVPGOTVA TVPGONVA TSI	F-11 	F12
PAN18_4750/1-291 Q78_18315/1-296 K0X_23800/1-297 SOD_c19210/1-288 VP1_T20/1-282 PP1Y_Mp16922/1-301 ETA_04540/1-307 PP1_3322/1-302 ETA_04540/1-307 PP1_3322/1-301 PP1_3349/1-304 H045_11530/1-304 H045_11530/1-304 PFL_3349/1-304 PFL_3349/1-304 ESA_01347/1-288 ROD_13341/1-301 ECENIK4_138221-302 Acav_45321/-291	80 GT VYNVGSTVF SA - VYNQGDTI SP AYQOGVI QY AYSVGQTI INN - A I AIGNVI INN - AI AIGNVI TA TYAVGSTI ASNSEVQISKTY ST ELI IGGTAI TY PI TRGVGYT SF PI ARNTGFI SF PI ARNTGFI SF PI ARNTGFI SF PI ARNTGFI SF PI ARNTGFI SF PI ANTGFI SF PI ANTGFI ANT	L WSSTT WSSTT WSRTT YSL YSL YSSL SST WSSTT WSSN FRTG FRTG FRTG FARNG FARNG FGTGG FTDTD FARNS VINSAT NYSQAQ WSGS WSGN MSGS WSGN INSG	80 	02 - LG LG L - LL SL I -	100 NAT	E11 - DGS L - NST L - DGT M - NNNF - SANL - GGT L - GYN - VF P - TYAKT - VF P - TYAKT - VF F - TYAKT - NF AI - NF	E12 PLYL PLYL PLYV PLYL PLX PLX PLX PLX PLX PLX PLX PL	110 TAT	F-11 	F12 130 - GL NWAWH- - P I SWTWN - - T I TWVYR - - NL TWNYH - NL TWNYH - SI DYTWH- - SI DYTWH- - SI LWWYN - NVEWTWK - NL AWMYN - NL AWMYN - NI AWWN- - NI AWWN-
PAM18_4750/1-251 QTS_18315/1-256 KOX_23800/1-297 SOD_c19210/1-283 VP_1720/1-282 PP1Y_MpI6922/1-301 ETA_04540(1-307 PP4_34580/1-300 PP4_34580/1-300 PP4_34580/1-300 PP5EIN3342/1-301 H045_11530/1-304 M634_169771-302 PFL_3484/1-304 PAGR_g0744/1-305 ECS_38210/1-306 ESA_01347/1-288 ROD_13341/1-301 ECENIK_13225/1-302 ECENIK_13225/1-302 BMASAVP1_A1401/1-294 ROD_054_12-1291 BMASAVP1_A1401/1-294 ROD_054_12-1291	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYSUGGTIS QY - AYSVGGTIS QY - AYSVGGTIS QY - AYSVGGTIS QY - AYSVGGTIS ST - ELTIGGTAT TY - PITRGVAPY ST - ELTIGGTAT TY - PITRGVAPY SY - PITRGVAPY SS PIARNTOFF SS PIARNTOFF AN - ELTIGGSAF AT - ELAVGGVTT PSGSELAINGSYT ASSNEVGISKSTY ASSNEVGISKSTY SSSEVGISKSTY SS CILLV SY TO SLUSS	L-WSSTT WSRTT WSRTT YSSL YSSL YSSL YSSQ FRTG FARNG FARNG FARNG FARNG FARNG FARNG FARNG FARNG SCGTGG WIGG WSGS WSGS WSGS WSGC	90 F	02 	100 NAT	E11 - 065 L - NST L - 06T M - NNNF - SANL - 66T L - 67 L - 78 AV -	E12 PLYL PLYL PLYF PIYI PIYI PIYI PIYI PIYI PIYI PIYI PI	110 TATGVTL P	F11 	F12 130 - GL NWAWH- - P I SWTWN - T I TWVYR - NL TWNYH - NL TWNYH - SI DWTWH - SI DWTWH - SI DWTWH - SI LWWYN - NL AWWYN - NI AWSWN - NI AWSWN - NI AWSWN - NI AWSWN - NI AWSWN - NI AWSWN - SI LWSWN - NI LWSWN - NI LWSWN - NI LWSWN - TT AWWYS - TT
PAM18_4750/1-291 QTS_15315/1-296 (XO_23800/1-297 SOD_c19210/1-288 VP_1720/1-282 PP1Y_M0J6922/1-301 Entas_2592/1-302 Enta_34580/1-307 PP4_34580	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYSUGGVIS QY - AYSVGGTIG SP - AALDIGKLI XY - PITRGYGFIG SP - ALPIGKLI RY - PITRGYGFI SY - PITRGYGFI SY - PITRGYGFI ANN - ELTIGGSAT ASSEVOISKSYT SSI - RANGGSYT ASSEVOISKSYT SI KLDGVTM SI KLDLGVTM SI KLDLGVTM	L-WSSTT WSRTT YSSL YSSL YSSL YSSL YAGNS WSSN FARNG FARNG FARNG FARNG FARNS YNSSAT YSSAQ WYSGS WSSN INASGQ WASGQ	80 F A N S F L 	02 	100 NAT	E11 - DG SL - NST - DG JM - NST - DG JM - NST - SANL - GG JL - GYN - TPKAV - SFKTV - VEF - TVAKTV - NFA - SFKTV - VEF - TVAKTV - NFA - RYTF - RFTL - RYTF - RFT - RFT - RYTF - RFTN - TASV - AOTL - AOTL 	E12 PLYL PLYF PLYF PLYF PLYF PLYF PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYF P	110 TAT	F-11 	F12 10 -GLNWAWH- -PISWTWN- -TIIWWYR- -NLTWNYH- -NLTWNYH- -SIDWTWH- -SSUFTYR- -SVLFTYR- -NUAWWYN- -NLAWWYN- -NLAWWYN- -NLAWWYN- -NLAWWYN- -NLAWWYN- -NILWWYN- -NILWWYN- -NFSWYS- -NFSWYS- -NFSWYS- -NFSWYS- -NFSWYS- -NFSWYS- -NFSWYS- -NFSWYS- -TIAWWD- -TIAWWD- -TIAWWD- -SILWWA- SILWWA- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILW- -SILWW- -SILW- -SILW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILWW- -SILW- -SILW
PAM18_4750/1-291 Q75_15315/1-296 (KOX_23000/1-297 SOD_c19210/1-288 VP_1720/1-282 PP1Y_Mp18692/1-301 Entas_2592/1-302 Ent45450/1-302 Pp4_34580/1-302 Pp4_34580/1-302 Pp4_34580/1-304 Pp4_5155/1-302 Pp4_3458/1-304 PAGE_0074/1-305 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-288 ROD_139341/1-301 ECENHK_13255/1-302 Acav_45321/-291 BMSAVP1_A1401/1-294 BPC006_116821/-294 MOS_27712/1-282	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYOGGVIS QY AYSVGGTII NN AI AIGNVI TA TYAVGSTII ASNSEVQISKTYI ST ELI IGGTAI TY PI TRGTGFF SP ALVFIGGKLI SF PI ARNTGFI SF PI ARNTGFI SF PI ARNTGFI SF PI ARNTGFI SF PI ARNTGFI AN ELI IGGSAI AT EI AVGGVTI PSGSEL AINGSYF ASNSEVISKSYI SY TG GLUY SI KLDLGVTYF NG ALVAGQAQC NN ALI ALGNVI	L WS STT	80 F.A.A. L.N.S. F.C.S.S. F.C.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S.S.	02 	100 NAT	E11 OG SL NST L OG TM NNNF SANL GGT L Q'NI TPKAV NANL TPKAV SPKTV NANL TPKAV SPKTV NANT NFSI RTTL RTTL RTTL AGT L SANL SANL	E12 PLYL PLYF PLYF PLYF PLYF PLYF PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYL PLYF P	110 TTATGVTLP PYASSNLA TTPGANVR TTGSSSNLA TTPGANVR TGSNNAINVNVS TGSNNAINVNVS TGAGTQYA TQAGTQYA TQAGTQYA TQAGTQYA TQAGTQYA TQAGSNYA TQAGSNYA TQISSNYA TQISSNYA TQIGSNYA TQIGSNYA TQIGSNYA TYY	F-11	F12
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_c192101-283 VP_17201-282 PP1Y_MpJ69221-301 ETA_045401-307 PP4_345801-300 VF153561-302 Ppu_3332/1-301 H045_115301-304 M634_169731-302 PFL_33491-304 H045_115301-304 M634_169731-302 PFL_34941-304 ESA_0113471-288 END_133411-301 ECEN1K_138251-302 Acav_45321-291 BMASANP1_A14011-284 BMC061_16821-294 MDB_271217-288 VPC_212511-282	80 GT VYNVGSTVF SA - VYNQGDTIS SP AYSUGGTIS QY AYSVGGTIG ASNSEVGISKTY ST ELTIGGTAT TY PITRGVAFI SY PITRGVAFI SF ALNRNTOFIC AN ELTIGGSAF AN ELTIGGSAF AN ELTIGGSAF ASNNEIALGSYT ASSSEVGISKSTY SSSEVGISKS SSSEVGISKSTY SSSEVGISKSTY SSSEVGISKSTY SSSEVGISKSTY SSSEVGISKSTY SSSEVGISKSTY SSSEVGISKSTY SSSEVGISKSTY SI KLDLGYTY NN ALAGONOVI GY AYSGGTIGT	- WSSTT. WSSTT. WSRTT. YSSL. YAGNS. WSGN. TYSQSQ. FRTG. FARNG. FGGGGG. FARNG. FGGGGG. FTDTD. FARNS. VNSAT. NSGAQ. INASG. WSGQ. LNASG. WASQQ. LNASG. MAGNS. SSL	90 F	02 - LG LG L - LG LG L - LG LG L - LG LG L - LL SL L - L - LL SL L - L - LL SL L - L - LL SL L - L - L - L - L - L - L - L -	100 NAT	E11 OGSL NSTL OGTM NVNF SANL GGTL GVN VFP TVAKTV OFF TVAKTV OFF TVAKTV NANL TPKAV SPKTV OFF TVAKTV NFAI NFAI NFAI NFAI AGTL RYNF AGTL AGTL NSAI SANL NNF	E12 PLYLE PLYVE PLYVE PLYF PLYF PLYF PLYF PLYLE PLYF PLYF PLYF PLYF PLYF PLYF PLYF PLYF	110 TAT	F-11	F12 130 - GL NWAWH- - P I SWTWN - - T I TWVYR - - NL TWNYH - NL TWNYH - SI DYTWH- - SI DYTWH- - SI DYTWH- - SI LWWYH - NL AWWYD - - NI AWWN - NI AWWN - NI AWWN - NI SI NYN - NF SI NYN - TF SI NYN - TF SI NYN - TF SI NYN - TI AWWD - TI AWWD - SI LWWYD - NL NWNYD - NL NWNYH - NL NWNH - NL NWH - NL
PAM18_4750/1-291 QTS_18315/1-296 KOX_23800/1-297 SOD_c192101/288 VP_17201-282 PP1Y_MpI69221-301 ETA_04540/1-307 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PFL_3349/1-301 PFL_3349/1-304 PFL_3349/1-305 PFL_3349/1-238 PFL_349	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYSUGGVIS QY - AYSUGGVIS ST - ELTIGGTAI TY - PITRGVAFI SY - APISGVAFI SY - PITRGVAFI SY - PITRGVAFI SY - PITRGVAFI ANNEIALGGSYI ASSNEIALGGSYI ASSNEIALGGSYI SS - KLDLGVTY SI - KLDLGVTY	L-WSSTT. WSSTT. WSRTT. YSSL. YAGNS. WSSTT. WGGN. TSS. FARNG. FGTGG. FTDTD. FARNG. FGTGG. FTDTD. FARNS. VNSAT. NYSAAQ. WTGO. WSGS. WSGS. WSGC. LNASG. LNASG. LNASG. SSL. WASGQ. LDA1. YAGNS. SSL. WSSTT. SSL. WSSTT. SSL. SS	90 F - A - A - A - A - A - A - A - A - A - A	02 	100 NAT SGP NSG SGP SGS GGF NGS GGF GGP GGP GGP GGS GGS GGS GGP GGP GGP GGP GGP GGP GGP GGP GGP GGP	Ei1 DGSL NSTL OGTM NVNF SANL GGTL QYNI VFPI TPKAV NANL TPKAV SPKTV SFKTV NANL TPKAV SFKTV NANL TPKAV SFKTV NANL TFKAV SFKTV NFSI RVTF RVTF RVTF RVTF SANL NFSI SNT SANL NFSI SNT SANL NFSI SNT SNT SNT	E12 PLYLE PLYLE PLYPE PLYF	10 TATGVTLP PVASSNLA TATGANVP TGSNNAINVNVS TGSNNAINVNVS TGSNNAINVNVS TGAGANVP TYAGANVR TGSNNAINVNVS TGAGANVA TVAGONVT TLPNAVVP TLINANVA TGNAVISTNIS TOIGSNVA TVYGANVA TLTGSNVA TVAGONVA TLTGSNVA TVAGONVA TVAGONVA TVAGONVA TVQGSNVA TVQGSNVA TVQGSNVA TVQGSNVA TVQ	F-11 	F12 10 -GLNWAWH- -PISWTWN- -NISWTWN- -NLTWWYR- NLTWWYR- -NLTWWYR- -SIDWTWH- -TFSINYN- -SVLFTYR- -NVEWTWK- -NLAWWYN- -NLAWWYN- -NIAWWYN- -NIAWWW- -NIAWWW- -NFIVAYN- -TYNWTYAN- TIAWWWD- TIAWWWD- -TLAWWWD- -SLRWWA- SLRWWA- -NLAWWYA- -NLAWWY- -NLAWW- -NLAWW- -NLAWW- -NLAWW- -NLAWW- -NLAWW- -NLAW- -NLAWW- -NLA
PAM18_4750/1-291 QTS_15315/1-296 (KOX_23800/1-297 SOD_c19210/1-288 VP_1720/1-282 PPTY_M91692/1-301 Entas_2592/1-302 Enta_52592/1-302 PPt_34580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_34580/1-307 PP4_34590/1-307 PP4_3491/1-301 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-305 EGX_074/1-291 PG	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYSUGGTIS QY - AYSUGGTIS SP - AYSUGGTIS ST - ELTIGGTAI TY - PITRGYAFI SY - PIRGVAFI SY - PIRGVAFI SY - PIRGVAFI ASSEVOISKSYT SSI - KLDGYTY SI KLDGVTY SI KLDGVTY SI KLDGVTY SI KLDGVTY SI KLDGVTY SI	L WSSTT. WSSTT. WSRTT. YSSL. YAGNS. WSSTT. WSCN. FARNG. FARNG. FARNG. FARNG. FARNG. FARNS. VNSAT. NYSCAO. WTGO. WGO. WASCO. LDA1. YAGNS. YSSL. WSSL. WSST. SST.	80 FA. L. N. S. F. S. I. I. I. L. L. L. L. L. E. S. N. K. S. S. S. S. S. S. S. S. S. S. S. S. S.	02 	100 NAT	E11 - DG SL - NSTL - DG TM - NVNF - SANL - GG TL - Q'NI - VF PI - TPKAV - NANL - TPKAV - VEF - TVAKTV - VEF - TVAKTV - VEF - TVAKTV - NFAI - RFTL - RFTL - RFTL - RFTL - RFN - NSAI - SANL - NNF - NSAI - SANL - NNF - OGTM - SANL - NNF - OGTM - OGTM - OGTM - OGTM - OGTM - OGSL - OGNL -	E12 PLYL PLYL PLYV PLYY PLYY PLYI PLYI PLYL P	110 TAT	F-11	F12 100 - GL NWAWH- - PI SWTWN- - TI TWWYR- - NL TWWYH- - NL TWWYH- - SI DWTWH- - TFS INYN- - SI DWTWH- - TFS INYN- - NL AWWYD- - NI AWWND- - NI AWWND- - NI AWWND- - NI LWWN- - NFS VNYS- - NFS VNYS- - NFS VNYS- - NFS VNYS- - TFS INYN- - TT AWWDD- - TI AWWDD- - TI AWWDD- - NL AWWYD- - NL AWWD- - TI AWWDD- - NL AWWD- - NL WWYD- - NL IWWYD- - NL IWWYD- - NL IWWYD- - NL IWWYD- - NL WWDY- - NL WWYD- - NL WWD- - NL WWYD- - NL WWYD- - NL WWD- - NL
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PAM18_4750/1-291 QTS_15315/1-296 KOX_23800/1-297 SOD_c19210/1-288 VP_1720/1-282 PP1Y_MpI692/1-301 Etta_2529(1-302 Etta_2529(1-302 Etta_2450/1-302 PP4_3450/1-302 PP4_3450/1-302 PP4_3450/1-302 PP4_3349/1-301 H045_11530/1-304 H045_11530/1-304 PP5EEN334/1-301 H045_11530/1-304 PFL_3349/1-304 PFL_3349/1-304 PFL_3349/1-305 ESA_01347/1-298 ROD_1934/11-301 ECENIK_113825/1-302 Aca:v_45521/1-298 BMC30/PT_41401/1-294 BPC006_11652/1-294 MWWW4_1c121201/-288 ECA30771-297 NCGM2_0934/1-291 BJAB0068_02454/1-312 BJAB0068_02454/1-312 BJAB0068_02454/1-312 BJAB0068_02454/1-312 BJAB0068_02454/1-312 BJAB0068_02454/1-300 P756_5011/289 P756_5011/289	80 GT VY NVGST VF SA - VY NQGDT IS SP AY SUGGV IS QY AY SVGGT IG QY AY SVGGT IG QY AY SVGGT IG QY AY SVGGT IG ST ELT IGGTAI TY P IT RGY GFI SY AP I TRGY AFI SY P I ARNTOFI SY P I ARNTOFI SY P I TRGY AFI SY P I TRGY AFI SY P I ARNTOFI SY P I ARNTOFI SSE LA INGSYT ASSNEI ALGGSYT ASSEVGI SKSTY SY C - GLLV SI KL DLGVTYH SI KL DLGVTYH SI KL DLGVTYH SI	L WSSTT WSSTT WSRTT YSSL YSSL YSSL YSS FARNG FARNG FARNG FARNG FARNG FARNS YNSSAT WSGS WSGG WSGG WSGG WSGG WSGG WSGG WSGG WSSG	90 F	02 	100 NAT	E11 - DG SL - NSTL - OG TM - OG TM - OG TM - OG TM - OG TM - OYNT - SANL - G TL - OYNT - TPKAV - OYNT - OYNT - OTM - OYNT - OTM -	E12 PLYL P	10 TATGVTLP PVASSNLA TATGANVR TGSNNAINVNVS TGSNNAINVNVS TGAGOVA TVAGANVR TGAGNVR TGAGNVR TVAGANVR TVAGANVR TVAGNVA TLPNAVVP TLINANVA TGSNVA TVYGSNVA TVYGOTVA TVAGOTVA TVAGONVT TVAGONVT TVAGONVA TVQ TST	F:1 120 AGTYT DTI. AGTYT DVL. SGTYT DVL. SGTYT DVL. SGTYT DVL. SGTYT DVL. SGTYT DVL. AGTYT DVL. SGTYT DVL. AGTYT DVL. AGTYT DVL. AGTYT GQL. AGTYT GQL. AGTYT GQL. AGTYT GQL. AGTYT TSTI. AGTYT TSTI. AGTYT GQL. AGTYT TSTI. AGTYT TSTI. AGTYT TSTI. AGTYT TSTI. AGTYT TSTI. AGTYT TVNL. AGTYT TVNL. AGTYT TVNL. AGTYT TTT. AGTYT TTTT. AGTYT TTTT. AGTYT TTTT. AGTYT TTTT. AG	F12 130 - GL NWAWH- - PI SWTWN- - TI I SWYWY- - NL TWNYH- - NL TWNYH- - SI DWTWH- - TS I SI NYN- - SS LL SWYN- - NL AWWYN- - NL AWWYN- - NL AWWYN- - NL AWWYN- - NL AWWYN- - NI LAWWYN- - NS LL WSWN- - NF NYA XN- - NF NYA XN- - TF SI NYN- - TF SI NYN
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PAM18_4750/1-291 QTS_18315/1-296 KOX_23800/1-297 SOD_c192101-283 VP_17201-282 PP1Y_MpI69221-301 ETA_045401-307 PP4_3458011-300 PP4_3458011-300 PP4_3458011-300 PP4_3458011-301 H045_115301-304 M053_16971-302 PPE_33491-304 PAGR_g07441-305 EC382101-306 ESA_013471-288 ESA_013471-288 ESA_013471-288 ECA30771-297 DBM25472-191 BMA5AXP1_A14011/294 MD5_2712/1-298 BMA5AXP1_A14011/294 MD5_2712/1-298 PF0_201512-297 P795_051011-297 P705_051011-297 P705_0510	80 GT - VYNVGSTVF SA - VYNQGDTIS SP - AYSUGGTIS QY - AYSVGGTIS ST - ELTIGGTAT TY - PITRGYAF SY - AYSVGGTIS SY - PITRGYAF SY - PITRGYAF AN - ELTIGGSAF SY - PITRGYAF AN - ELTIGGSAF AN - ELTIGGSAF AT - ELAVGGYTT ASSNEVGISKSTY SSEVGISKS SY - TORGVAF ASSNEVGISKSTY SSEVGISKSTY SSEVGISKS GT - LYNISGSTIG GT - LYNISSTY SST - SST AGSSTTNOTSIN SST SSE ASSTTNOTSIN SSE ASSTTNOTSIN SSE ASSTTNOTSIN	L WSSTT WSSTT WSRTT YSSL YSSL YSSL YSSL YSSL YSSS FARNS FARNG FARNG FARNG FARNS FARNS FARNS YNSSA WSSS WSSS WSSS WSSS WSSS WASGO INASGO YSSL WSSSS WSSS WSSSS WSSS WSSSS WSSSS WSSSS WSSSS WSSSS WSSSS WSSSS W	90 	02 	100 NAT	E11 - DG SL - NSTL - OGTM - NVNF - SANL - GGTL - Q'NN - VF P1 - TPKAV - NANL - TPKAV - VF P1 - TPKAV - VF P1 - TPKAV - SANT - VF P1 - TPKAV - SANT - SANT	E12 PLYL P	10 TAT YA SNLA YA SNLA YA YA SNLA YA SNA TGA GANVP TGA TGA TYA GANVP TTA GANVNVS TGA TVA GANVY TL TAT GANVA TQA GSNVA TGNOVISTNIS TGNOVIS TGNOVIS TGNOVIS TGNOVIS TGNONP	Fi1 120 AGTYT DYL AGTYT DVL SGTYT DVL SGTYT DVL AGTYT DVL SGTYT DVL AGTYT DVL AGTYT DVL AGTYT DVL AGTYT DVL AGTYT DVL AGTYT GQL AGTYT GQL AGTYT GQL AGTYT DVL AGTYT DTL AGT	F12 10 -GL NWAWH- -PI SWTWN- -NL NWNYD- -NL NWNYD- -SI DWTWH- -SI DWTWH- -SI DWTWH- -TF SI NYN- -SVL FTYR- -NVL WWYN- -NVL WWYN- -NI AWNWN- -NI AWNWN- -NI AWNWN- -NI AWNWN- -NI SUWS- -NI LWWYN- -NF NVAN- -NF NVAN- -TF NWY- -SI LWWY- -TI AWNWD- -TI AWNWD- -T
PAM18_4750/1-291 QTS_18315/1-296 KXO_23800/1-297 SOD_c192101-288 VP_17201-282 PP1Y_MpI69221-301 ETA_04540/1-307 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_345001-300 PP4_34501-300 PP4_34501-300 PP4_34501-300 PP4_34501-300 PF5_65101-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 PF5_6511-327 P	80 GT - VYNVGSTVF SA - VYNQGDTIS SP - AYODGVIS QY - AYSVGOTIG ST - ELTIGGTAT TY - PITRGYAF SY - PIRGYGT SF - ALPIARNTOF SF - PIARNTOF SF - PIARNTOF SF - PIARNTOF ASSEVOISKUNGST ASSEVOISKOTIG ASSEVOISKOTIG GT - VYNKOSTV NN - AIAIGONYI SI - KLDLGVTYN SI -	L WSSTT WSSTT WSRTT YSSL YSSL YSSL YSSL YSSL SSTT SSTT SSTT SSTT SSTT SSTT FARNG FARNG FARNG FARNG FARNG FARNG FARNG FARNG FARNG FARNG FARNG FARNG SSTT SSTT WSSS WSSG WSSG WSSG WSSG WSSG SSTT SSSTT SSSS	90 	02 	100 NAT	E11 - DG SL - NSTL - DG TM - NVNF - SANL - GG TL - Q YNI - TPKAV - NANL - TPKAV -	E12 PLYL PLYL PLYL PLYF PLYF PLYF PLYL P	10 TATGVTLP	F-11 120 AGTYT DTI. AGTYT DVL. SGTYT DVL. AGTYT DVL. AGTYT DVL. AGTYT GVL. AGTYT GVL. AGTYT GVL. AGTYT DVL. AGTYT TOVI. AGTYT TOTI.	F12 100 - GL NWAWH- - PI SWTWN- - NL SWTWN- - NL SWTWH- - SI DWTWH- - TF IS INYN- - SS LI SWTWH- - TF SI NYN- - SS LI SWWN- - NL AWWYN- - TY AWSWD- - NI AWWWN- - NI AWWWN- - NI AWWWN- - NI AWWWN- - NI AWWWN- - NI LWWYN- - NF NVAS- - NF NVAS- - NF NVAYN- - TF SI NYN- - SL RWWH- - TI AWWWD- - TI AWWWD- - TI AWWWD- - TI AWWWT- - NL IWNYH- - TL WWYH- - TF NYSF - NL IWNYH- - SUR SF SI NY- - NL IWNYH- - TF NYSF - NL IWNFY- - NL
PAM18_4750/1-291 QTS_15315/1-295 KOX_23800/1-297 SOD_c19210/1-288 VP_1720/1-282 PPTY_M01692/1-301 Entas_2592/1-302 Entas_2592/1-302 Entas_2592/1-302 PPt_34850/1-307 PP4_34850/1-307 PP4_34850/1-307 PP4_34850/1-307 PP4_3491/-307 H045_11530/1-304 M634_16975/1-302 PPL_34941-304 PAGR_075/1-302 PPL_34941-304 PAGR_075/1-302 PAGR_075/1-302 ESA_01347/1-298 ESA_0134	80 GT VYNVGSTVF SA - VYNQGDTIS SP - AYQDGGVIS QY - AYSVGGTIG ST - ELTIGGTAT Y - PITRGYAFI SY - PITRGYAFI SY - PITRGYAFI ASNEVGISKSYT SY - TO - GLUV SI KLDGVTIY SI KLDGVTIY SI KLDGVTIY SI KLDGVTIY GT VYNVSSTVF YNNSTSY GT VYNVSSTVF	L WSSTT WSSTT WSRT YSSL YAGNS WSRT WSRT WSRT WSSN FARNG FARNG FARNG FARNG FARNG FARNG FARNG KSS FARNG.	90 	02 	100 NAT	E11 - DG SL - NST - DG TM - NVNF - SANL - GG TL - QVN - TPKAV - SANL - TPKAV - SFRTV - VEF - TVAKTV - NANL - NNF - DC - DC	E12 PLYL P	110 110 TYAT	F:1 120 AGTYT DTI. AGTYT DVI. AGTYT DTI.	F12 130 - GL NWAWH- - PI SWTWN- - TI SWTWN- - NL TWNYH- - NL TWNYH- - SI DWTWH- - TFS INYN- - SI DWTWH- - TFS INYN- - NL AWWYN- - NI LWWYN- - NF SVNYS- - SL SVNYS- - SL SVNYS- - SVR SVNYS- - SVR SVNYS- - SVR SVNYS- - NF SVNYS- - SVR SVNYS-
PAM18_4750/1-291 Q75_18315/1-296 KXX_23800/1-297 SOD_c19210/1-283 VP_1720/1-282 PP1Y_MpJ6922/1-301 ETA_04540/1-307 PP1_3322/1-301 ETA_04540/1-307 PP1_3322/1-301 PP1_3322/1-301 PP1_3324/1-301 H045_11530/1-302 PFL_3349/1-304 H053_11571-302 PFL_3494/1-304 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_01532/1-302 EXA_0152/1-302 EXA_0152/1-302 EXA_0152/1-302 EXA_0152/1-302 EXA_0152/1-302 EXA_0152/1-302 EXA_0152/1-305 EXA_0152/1-305 EXA_0152/1-305 EXA_0152/1-305 EXA_0152/1-305 EXA_0152/1-305 EXA_0152/1-305 EXA_0152/1-305 EXA_001-328 EXA_001-	80 GT VY NVGSTVF SA - VY NQGDT IS SP - AY SUGGT IS QY - AY SUGGT IS ST - ELT IGGTAL SS - AY SUGGT IS SY - P I SRGVAFI SY - P I SRGVAFI SY - P I SRGVAFI SS - EVFGOLHT SY - P I SRGVAFI AN - ELT IGGSAFA ASNSELA INGSYT ASSEVO ISKSTYT SSEVO ISKSTYN SY - TO - GLLV SI - KLDLGYTY NNA - ALVAGOAQC MN - ALVAGOAQC GT - L'NN INSTYT SI - KLDLGYTY NNA - ALVAGOAQC GT - L'NN INSTYT SI - KLDLGYTY SI - KLDLGYTY SI - KLDLGYTY SI - KLDLGYTY NNE I I SLGGEKI SGC <	L WSSTT WSSTT WSRT YSL YAGNS WSRT WSST FARNG FATTG FARNG FARNG FARNG FARNG FARNG FARNG FARNG KYSA WTGQ WTGQ WSGN WSGN WSGN WSG WSGO WSST WSST WSST WSST WSST WSST WSST WSST WSST WSSS	90 	02 	100 NAT SGP NSG SGP GGP GGS GGG GGG GGG GGS GG GG	E11 DGSL NSTL GGTL OGSL NVNF SANL GGTL OVNF TPKAV SRKTV GGTL TPKAV SRTV GGTL TPKAV SFKTV GGTL TPKAV GGTL TPKAV GGTL TFKAV GGTL TFKAV GGTL TFKAV GGTL TFKAV GGTL NFSI RFTL RFTL RFTL RFTL RVTF FFTL RFTL GGTL OGNL SFKTV GGTL SASSTV SASTSV SASSTV SASSTV SASSTV SASSTV SASSTV SASSTV SASSTV SASSTV SGSRTL GGTVASSTV SGSRTL GATVASTO SGSRTL GATVASTO SGSRTL GATVASTO SGSRTL SASSTV SGSRTL SASSTV SGSRTL SASSTV SGGSTT SAMLASTTO SGGSTL SASSTV SGGSTL SASSTV SGGSTL SAMLASTC SGGSTL SAMLASTC SAMLASTC SGGSTL SAMLASTC SGGST SAMLASTC SGTATTASTC SGGST SAMLASTC SGTATTASTC SGGST SAMLASTC SGTATTASTC SGGST SAMLASTC SGTATTASTC SGGST SAMLASTC SGTATTASTC SAMLASTC SGTATTASTC SGGST SAMLASTC SGTATTASTC	E12 PLYL PLYL PLYV PLYF PIYI PIYI PIYI PIYI PIYI PIYI PLYL PIYL PLYL PLYL PIYI PLYL PIYI PLYL PIYI PLYL PLYF PLYL PIYI PLYL PIYI PLYL PIYI PLYL PIYI PLYL PIYI PLYL PIYI PLYL PIYI PLYL PIYI PLYL PIYI PLYL PLYL PLYL PIYI PLYL PIYI PLYL PIYI PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYL PLYF PLYF PLYF PLYF PLYL PLYF PLYL PLYF PLYL PLYF P	110 TATGVÍLP	F:1 1 AGTYT DTI AGTYT DVI AGTYT DVI <td>F12 </td>	F12

	F12	G11	G12	A2		B2	C21
	* :140	* 150 160	170 18	* •:	** * *	**	• :
PAM18_4750/1-291	L CAAG I G P - '	190 190 /CVYD	DGTASSSVNVTLTVLKD	CFIDSAP-DLS	FGSAALVSAFTAV	- NQNIGVRCTLNAT	YTIGFDNGNNF-
Q7S_18315/1-296	MCSVAIGTLI	CL AD	SGNVSGNVALTLNVTNF	CYIDSAP - NVG	FGSAALPSGLTTV	VANTISVRCTLNAS	YSVNL TSSVPV -
SOD_c19210/1-288	ICG LGV LGI	CIWV	VDGVDKLSTMTITAVITKD	CLIGTAQ - NVN	FGSMA L VGQFNPV	- NQSITLTCTKTEG	YNTYFTNGNNP -
PP1Y_Mpl9692/1-301	LCA ISL FSI LCS AGAV T - I	- CL GG - P	- F SGTAT ST VT VKL T V SN D D <mark>G</mark> AT S ST L T V T M T V S A D	CVINSAP-NVN CVL-SAP-TAD	FGSYA L I TQFAPV FGSAA FVGSFDPV	- NQNISATCTKNAT - AQTITIRCTKDAS	FTTYITNGNNF - YTVGIDD <mark>G</mark> QNY -
Entas_2592/1-302	VCSVGILGI	CTTPQ	TGTATTSILLNMTVTND	CSAMTTP - DVN	FNSAP L VQNFPT I	- SQAIAVTCTKGST	YTIGINNGANA -
PP4_34580/1-300	YCDG - IGL GG		GTGTKPLTVTLTVTND	CQ-ITTP-NIS	FASAP VVAGFGTV	- SQGINVSCTKGSN	YTVGL DDGQNV -
YE1856/1-302 Pput_3332/1-301	ICKVLNVLG YCSG-IGALG	GC I G SWVG S	• GT <mark>GTD I SSVTVTL VVSKD</mark> • GSGSQVL NVSL TVTND	CAINSAS-DVN CQ-ITTP-DIS	FGSFA L VGQFNPI FASAP VVAGFGTV	- SQNITL TCTKGTT - SQGINVSCTKGSS	FNTYVTPGDNP - YTVGLGDGQNV -
PSEEN3394/1-301	YCSG - 1G I GNI	CLG-RDI	GSGNQSIVVSLTVTND	CQ-ITTP-NIS	FGSAP VVAGFGTV	- SQSVSLSCTKGST	YTVGL DDGQNV -
M634_16975/1-302	YCKG-VGLPG	CI I - RNE	GSAQSTITVELEVTPD	CM-ITAP-DID	FGSSP L VAGF DPV	- SQVISLTCTKNSS	FTIGLNDGVNA -
PFL_3949/1-304 PAGR g0744/1-305	YCSG-IGALG ICTS-VSALG	I CLG - RDV	<mark>G</mark> SGTQSLTVNMTVSND TGSGVIPITVTVVLSND	CV-ITAP-NIS	FGSAP VISAFATV FGSAP LVASFGAL	TGQTINLACTKGSA - SQTISVLCSKGST	YTVGLSD <mark>G</mark> QHPV YTVGLSNGNNA -
EbC_38210/1-306	ICTG-IGALG		T <mark>G</mark> SGT I P I T T T L I V T N D	CTTITAP - DIS	FGSAP LVSSFNTI	- SQSINVICTKGST	YTVGMSN <mark>G</mark> SHA-
ROD_19341/1-301	VCQIGALGI	- <mark>CG</mark> T AQ	- T <mark>GTVASSLQLNLTVTND</mark>	CITINAP - NUN	F <mark>GS</mark> AP LAKDFPAV	- SQAVSITCTKGSS	YTVGINNGNYA-
ECENHK_13825/1-302 Acav_4532/1-291	VCA VGL GSI ICEGLLGV GGI	CTSPQ	· - S <mark>GTATTSILLNMTVTND</mark> · - NGNVNRLLTVQLVVTND	CSAMTTP-DVN CT-LSAP-NVQ	FNSAP L VQSFPTV FGSAP L PAAFPAV	- SQAIAVT CTKGST - SGNVSVVCTRGLS	YTIGINNGANA - VTVGLGPGTYP -
BMASAVP1_A1401/1-294	YCSG-IGVLG	CLG-RDR	<mark>G</mark> SGTAVVPVTITVTND	CM-IAAP-DVN	FGAAP TVASFAPV	- TGSVSL TCTKGMV	YTVGL SS <mark>G</mark> ANPH
MDS_2712/1-298		CSWSRSPGL TQPCL A I CGPPN	WGT <mark>G</mark> SLATVTITLVVSKA	CRIDTLP-NVD	FGANA L I SQF SA -	QQRTFAVTCTNTEG	YTLSFDNGQNY -
YPC_2125/1-292 SMWW4 v1c21200/1-288	LCA ISL FSI	CLGGR	FS <mark>G</mark> TATSTVTVKLTVSND	CVINSAP - NVN	FGSYA L I TQ FAPV	- NQNISATCTKNAT	FTTYITNGNNF - YNTYFTNGNNP -
ECA3077/1-297	LCALGILG-I	CSYD	E <mark>G</mark> STTSTLNITMTITND	CQITSAP - NIS	FGTAA FPANFAAV	- NNNLGVRCTLLGA	YTVKLVSTHPD-
CsuE/1-312	YSVPAVAI VGIG'	/FFESPGFRRGALGIGFN	WGS <mark>G</mark> ADSL <mark>GSLSITVLPD</mark>	CR-ILAQ-DVN	FGTAA FASKLEPV	-QSSMGIRCSVNTP	YYVSLNNGLSPQ
BJAB0868_02454/1-312 A3UG 03070/1-299	YSVPAVAI VGIG' S ATROD - ALQ	/FFESPGFRRGALGIGFN	WGSGADSLGSLSITVLPD EGEOVOGGTNAOAEISOG	CR-ILAQ-DVN CYIERVT-PLN	FGTAA FASKLEPV FGTLSSTA - TLRPTRS -	- QS SMG I RCS VNTP - TATL TTRCPAGTA	YYVSLNNGLSPQ FTLAMGNGNHAS
P795_6510/1-297	MDL L GL :	GGDLLGG	-WDSGDTLLTANFVVPSL	CQLNSTS-TVD	FGNINDIGTTKRDYTA -	-QGAVNTTCNYGTP	YSIYLGDGNHRI
XCC1378/1-316	ESL IGIPP - APS	SCTAGGSG A	- TETDAFTYTSQASVAAH - KTASNAF <mark>PFTASANVP</mark> AR	CNTYVTT-DLD	FGT I AGS I TSNIDR -	- TSTVSLSCTNRTA	WNIGLAPSNEDT WNIGLGN <mark>G</mark> VNAS
XAC1424/1-316 VAPA 1c20560/1-308	ESI TGMPS - LPS: 0 - G S T - APS	SCTAGGTG S	KTASNAFPFTASATVPAR	CNAYVTT - DL D	FGSIAGS IDTAIDR -	- SSTISLACTNRTA	WNIGLDNGSNAS
Sinme_6943/1-295	L-LSS	OCT TA	AGT <mark>P</mark> ASPTFTVNATVAAN	CLV AVQNID	FGTKG - V L SANSDA -	- TGGVSVTCTPGTT	YTVSLNGGTTN -
Mesop_1922/1-295	K-TAS	ACPTG	SA - AGT VSF SATAT VAND SRQAT <mark>SSGSTWTAT I</mark> NAN	CNVS-AT-NVN	FGSVG - V LASNVDS -	- TGSVTVRCTDTTP	YNIGL SAGAGSG
BBK_506/1-296 Rta 34890/1-282	T L - APL	CASQ	SS-FGTFAFTASATVVND	CFIN-AT-NVA	F <mark>GSTG</mark> -VIQ <mark>G</mark> ALTA- EHYASEQAGPATA	- TGT I SAQCT NGDA	FRIAL NGGA S
BYI23_D012110/1-291	IGY S G - TPPI	NCATS	TAPYTTAPFLVTATVGSD	CDIS-AT-PMR	FANAR-LLRKPLLA-	- TSSLTVTCTAGLN	YAIEL DAGTTPG
ABO_0699/1-294 BRPE64_DCDS03180/1-302	LL-TAP:	SCNTTS	TANSNALSFTVSATVIND	CTLA-AT-NIN	FGTAG - V L NGTLNA -	- TGTL SVACT SNDP	YSIAL SAGSGSG
AXYL_05495/1-300 Smlt1510/1-323		CASL	TS-RGSYNFTVRANVTNN	CTIS-AN-PLN	FGSMA - D FRSARLA -	- NTTLAVRCTNNDA	YRIRLNGGQ N
OA238_c46250/1-288		CDQS	DPASAFTVSATLTTS	CTIN-VS-NMD	FGVIDTA IVAPVDQ -	- TATIEVSCTNASP	YTISIGSGLQPA
XOO1979/1-316	ESI TGVPP - APSI	NCT AGGSG S	· VATTEPETVSAAVTKQ · KTASNAE <mark>PETASANVP</mark> AR	CNTYVTT - DLD	FGSIAGT IDTAIDR -	- TSTISLACTNRTA	WNIGL DNGSNAT
	C22	* C2'/D2	D2'	* D2"	*• E2	*=	F21 F22
		* • •	*		** *		* *
DAM49 4750/4 204	230	240 * 250		270		300 G NV P - G T	
PAM18_4750/1-291 Q7S_18315/1-296	230 - SGG WRRM - SGQ YRQM	240 * 250 SGANAIQYNLYKPG ASTVGGT-TRYLQYQIFKG-	* 260 DSTVWTTSNTQAG DSTVWTASTDSSA	270 	280 <u>* *</u> 290 * SAAQNVPYRAIVNP - AD STSQSFPYTASVNL - AD	300 G NV PAG T S NQ PAG N	* * 310 YSDTVRVILTY- YSDMVTVTVTY-
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_c19210/1-288	230 - S <mark>G</mark> G W <mark>R</mark> RM - SGQ Y RQM - VGD WRQM - VTG W <mark>R</mark> QM	240 * 250 _ SQ ANA IQYNLYKPG - ASTVGGT - TRYLQYQIFK G SQP I ANQPTAWLQYQFYQPN XNGT SNFMQYQIYLPN SNFMQYQIYLPN	★ 260 DSTVWTTSNTQAG DSTVWTASTDSSA GSAWTESNNLSV TTVWDSTNKQSG	270 	280 * * 290 * SAAQNVPYRAIVNP - AO STSQSFPYTASVNL - AO SAAQSANYTLKINP - TO SAAQSIPYLAVINA - AO	300 G NVPAGT S NQPAGN S NQPAGT T EKPVGA	* * 310 YSDTVRVILTY- YSDMVTVTVTY- YSDTVLVTVSY- YQDNLSFVVEY-
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_c19210/1-288 YP_1720/1-292 PP1Y_M09602(1,301	230 - SGG - WR RM - SGQ - YR QM - VGD - WR QM - VTG - WR QM - VAP - WP RM - LG - RR	240 * 250 .SG ANA IOYNLYKPG SSTVGGT -TRYLOYOIFKG SOPIANDOYOFYOPN NGTSNFMOYOIVLPN (LTSG -TDYLOYOLYOGA NA GSYLAFELYPPOG.	* 250 DSTVWTTSNTQAG OSTVWTASTDSSA GSAWTESNNLSV TTTVWDSTNKQSG GVIPWNVTNKRTS GVIPWNVTNKRTS STSRWGHLGTERRSSGE	270 	280 * * 290 * SAAQNVPYRAIVNP - AD STSQSFPYTASVNL - AD SAAQSANYTLK INP - TO SLAQSIPYLAVINA - AO STQQL IPYNAVINP - QO STQQL IPYNAVINP - QO TDQTYTYRAFILS - GO	300 G NV PAGT S NQ PAGT S R PVGA T	* * 310 YSDTVRVILTY- YSDTVLVTVSY- YQDNLSFVVEY- YQDNVSVVLEY- YTDTITVDVFF-
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_c19210/1-288 YP_1720/1-292 PP1Y_Mpi692/1-301 Entas_2592/1-302	230 - SGG - WRRM - SGG YROM - VG D - WROM - VAP - WROM - VAP - WROM - LG I RL - LNN - VRRM	240 * 250 .SG ANA IQ'NLYKPG STVGGT -TRYLOYOIFKG SGP IANOPTAWLOYOFYOPN (NGT SNFMOYOIVLPN (LTSG -TDYLOYOLYOGA NA GSY IAYE IYPOG 	* 260 DSTVITTSNTQAG DSTVITASTDSAG GSAWTESNNLSV GSTVITSNKQSG GVIPVNVTNKRTS STSRWCHLGTERRSGE TSRWCHLGTERRSGE	270 	280 * 290 * 320 * 290 * 315 QS F PYTAS VN - 40 34 AQ SANY LK INP - TO 14 QS IPY LAVINA - A0 31 QQ I IPY NAVINP - 00 31 QQ I IPY NAVINP - 00 11 DQ TY IY RAE ILS - 60 LL RTY NY TAK VL T - NO	30 G	* * 310 YSDTVRVILTY- YSDMVTVTVTY- YSDTVLVTVSY- YQDNVSVVLEY- YDTLTVDVEF- YSDTLIVDVAF-
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/282 PP1_20/1-292 PP1Y_Mp19692/1-301 ETA_04540/1-307 PT4_34580/1-300	230 - SGG WR RM - SGG YR QM - VG WR QM - VTG WR QM - LG I RR L - LNN - VR RM - TGH - QR YM - SGG - RR RM K	240 * 250 .SG ANA IQ'NLYKPG SSTVGGT -TRYLQ'YQ IFKG .SG PIANQPTAWLQ'YQ FYQPN .KGT SNFMQ'Q I'VLPN .LTSG -TDYLQ'YQLYQGA ANA GSYIAYEIYYPQG .SS GNQLA'Q I'YQGS .SS GNQLA'Q I'KSA	* 260 DSTVWTTSNTQAG DSTVWTASTDSA GSAWTESNNLSV GSTVWTASTDSAG STSRWGHLGTERRSGE. STSRWGHLGTERRSGE. TNRWGGSGTERWASSA GPDWGDNGSAGARRSSTD. GVVRWGASGAARRSSTD.	270 	280 * 290 * SAAONYPYRAIVNP-AD STSOSFPYTASVNL-AD SAAOSANYTLKINP-TO SLAOSIPYLAVINA-AD STOOLIPYNAVINP-OO STOOLIPYNAVINP-OO LIRTYNYTAKULT-SO GSQUFNYNAKVYLT-SO	300 GNQPAGT SNQPAGT TEKPYGA AQKTVGT STPPAGT NTPAAGS ATPPAT	* * 310 YSDTVRVILTY- YSDMVTVTVTY- YSDTVLVTVSY- YODNLSFVVEY- YDTLTVDVEF- YSDTLIVDVAF- YSDTVIDVAF- YSDTVIDVAF-
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/282 PP1_Y_D19692/1-301 Entas_2592/1-302 ETA_04540/1-307 PP14_34580/1-300 YE1856/1-302 PP101_3321/3.301	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VTG - WR QM - LG I RL - LNN - VR RM - TGH - QR YM - SGG - RR RMK - VT WR QM 	240 * 250 .SG ANA IQ'NLYKPG SSTVGG	* 260 DSTVWTTSNTQAG DSTVWTASTDSA GSAWTESNNLSV STTTVWDSTNKQSG STSRWGHLGTERRSSGE. TTNRWGSGTERWASSA GPDWGDNGSAGARRSSTD. GVVRWGASGAARRSSTD. GTVRWGASGAARSSTD.	270 	280 * 290 * 280 * 290 * STAGNYPYRAIVNP-AD STSGSFPYRASVNL-AD STAGSFYTASVNL-AD STAGSTPYRASVNL-AD STAGSTPYRASVNL-AD STAGSTPYRASVL-AD STAGSTPYRASVL-SO LLRTYNYTAKVL-SO LLRTYNYTAKVL-SO SGVFNYNAKVVL-SO SAGUCVPFHAVINP-ND GSQVFNYNAKVVT-DO SAGUCVPFHAVINP-ND	300 G NVPAGT S NVPAGT S NVPAGT S CAT T CAT T CAT T TPAGT N TPAAT N CAT PAAT N CAT PAAT	* * 310 YSDTVRVILTY- YSDMVTVTY- SDTVLVTVSY- YODNLSFVVEY- YDTLTVDVEF- YSDTVLVLSF- YSDTVTVLSF- YSDTVTVLSF- YSDSVILDVGF- YRDNVSLVLVY- TDSVILDVGF-
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/282 PP1_Y_D[0950/1-301 Entas_2592/1-302 ETA_04540/1-307 PP14_34580/1-300 PE1856/1-302 PP14_34580/1-301 PSEEN3394/1-301	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VA - WR QM - LG I RL - LNN - VR RM - TGH - QR YM - SGG - RR RMK S - GG - RR RMK	240 * 250 .SG ANA IQ'NLYKPG SSTVGG	260 DSTVWTTSNTQAG DSTVWTASTDSA GSAWTESNNLSV STTTVWDSTNKQSG STSRWGHLGTERRSSGE. TTNKWGSG TERWASA. GPDWGDNGSARVFSSA. GVDWGDASGAARRSSTD. GVVRWGAGAARRSSTD. GVVRWGSLTTARRASDD	270 	280 * 290 * 280 * 290 * 270	300 G NVPAGT S NVPAGT S NVPAGT S TPPAGT N TPPAGT N TPPAGT N TPPAGT N TPPAGT N TPPAGT N	* * 310 SDTVRVILTV SDTVLVTVS CONLSFVEY CONSVVEY TOTLVVEY SDTUVVS SDTUVVS SDTUVVS SDSVILOVS FRNVSLVVY TOSVLDVGF TOSVLSVC TOSVC
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/-282 PP1	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VG - WR QM - LG I RR L - LN - VR RM - TG H - Q RYM - SGG - RR RMK S - SGG - RR RMK S - SGG - RR RMK S - SGG - RR RMK	240 * 250 SG ANA IQ'NLYKPG SSTVGG TRYLQ'Q IFKG SG PIANQPTAWLQ'Q GFYQPN (NGSNFMQ'Q I'VLPN (LTS SNFMQ'Q I'VLPN (LTS	* 260 DSTVWTTSNTQAG DSTVWTASTDSA GSAWTESNNLSV STSWGHLGTERRSSGE. TTVWDSGSGTERWASSA GPDWGDNGSARVFSSA GVDWGASGAARRSSTD. GVVRWGASGAARRSSTD. GVVRWGASGAARRSSTD. GAVRWGSLTTARRSSD. GTVRWGSLGAARRSSD.	270 	280 * 290 * 280 * 290 * STAGNYPYRAIVNP-AD STSQSFPYTASVNL-AD STSQSFPYTASVNL-AD STAGSTPYTASVNL-AD STAGSTPYTASVNL-AD STODLIPYNAVINP-00 STODLIPYNAVINP-00 STTOLIPYNAVINP-00 SGVFNYNAVYT-00 GSVFNYNAKVYT-00 GSVFNYNAKVYT-00 GSVFNYNAKVYT-00 GSVFNYNAKVYT-00 GSVFNYNAKVYT-00 SGVSFNYNAKVYT-00 SGV	300 G NVP AGT S NUP AGT S NUP AGT S FK PVGA A TP PAGT N TP PAGT N TP PAGT A TP PAGT A TP PAGT T TP PAGT	* * 310 ISDTVRVILTV SDTVLVTVS CONLSFVEY CONSVVEY TOTLVDVF SDTUVDVF SDTUVDVF SDTUVDVF SDSVILDVF FRNVSLVLVY TOSVILDVGF TDNVILDVGF VDNVLDVGF VDNVLDVGF VDNVLDVGF
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_c1921/01-288 YP_1720/1-292 PP1Y_Mple92/1-301 Entas_2592/1-302 ETA_04540/1-307 YE186/1-302 PP1W_332/1-301 PSEEN3394/1-301 H045_11630/1-304 M634_16375/1-302 PFL_3349/1-304 PAGR 07/44/1-305	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VA WR QM - VA WR RM - L NN - VR RM - L NN - VR RM - SGG - RR RMK S VGG - RR RMK S VGG - RR RMK S VGG - RR RMK S SGG - RR QM SAGG - RR QM 	240 * 250 256 ANA 10 YN LY KPG SST VGG TRY LOY 01 FK G- SG PI ANO PT AWL 0Y 0F Y 0PN (NG SN FMG Y 01 YL PN (LTS GS YI AY EI Y PPG G- NA GS YI AY EI Y PPG G- NG SNY MS DI YK EA TSG GS YI AY EI Y PPG G- SSA	260 DSTVWTTSNTQAG DSTVWTASTDSA GSAWTESNNLSV STSWGHLGTERRSSGE. TTVWOSGATERRSSGE. TINRWGSGTERWASA GPDWGDNGSARVFSSA. GVDWGDASGAARRSSTD. GVTRWGSGAARRSSTD. GVTRWGSAGAARRSSTD. GTVRWGSAGAARRSSTD. STERWGSAGAARRSSTD. SSDRWGSAGTERVGSAA	270 	280 * * 290 * 280 * 290 * STAGNYPYRA I VNP - AD STSQSFPYTASVNL - AD STSQSFPYTASVNL - AD STAGSTPYTASVNL - AD STAGSTPYTASVNL - AD STODL I PYNAV I NP - OD STODL I PYNAV I NP - OD STODL I PYNAV I NP - OD SGVFNYNAK V I T - DD GSOVFNYNAK V YT - DD STPONYNYRAC I MT - SD GSO I FNYNAR I WT - DD SSO I	300 G NVPAGT S NVPAGT S NVPAGT S TPPAGT N TPPAGT N TPPAGT N TPPAGT A TPPAGT A TPPAGT T TPPAGT S TPPAGT S TPPAGT	* * 310 (SDTVRVILTV (SDTVLVTVS) (SDTVLVTVS) (SDTVLVVS) (SDTVLVVS) (SDTVLVVS) (SDTVLVS) (SDTVLVS) (SDTVLVS) (SDVVLDVG- (SDVVLDVG- (SDVVLDVG- (SDVVLDVG- (SDVVLDVG- (SDVVLDVG- (SDVVLDVG) (SDVVD) (SDVD) (
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_c1921/01-288 YP_1720/1-292 PP1Y_Mple920/1-301 Entas_2592/1-302 ETA_04540/1-307 PP14_34580/1-300 YE1856/1-302 PP14_3421/-301 H045_11630/1-304 H045_11630/1-304 PFL_3349/1-304 PFL_3349/1-304 PFL_3349/1-304 PFL_3349/1-304 PFL_3249/1-306	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VA WR QM - VA WR RM - L NN - VR RM - L NN - VR RM - SGG - RR RMK S VGG - RR RMK S VGG - RR RMK S VGG - RR RMK S SGG - RR RMK S AGG - RR QM S AGG - RR QM SAGG - RR QM 	240 * 250 256 ANA 10 YN LY KPG SST VGG ANA 10 YN LY KPG SST VGG	260 DSTVWTTSNTQAG OSTVWTASTDSA GSAWTESNNLSV STSRWGHLGTERRSSGE. TTVWDSTNKQSG STSRWGHLGTERRSSGE. TTNRWGSGTERWASA GPDWGDNGSAGARRSSTD. GVVRWGSGAARRSSTD. GVVRWGSLTTARRASSD. GTVRWGSGAARRSSTD. GVVRWGSLTARRASSD. STERWGSVGAARRASST. SSDRWGPSGTERVGSAA.	270 	280 * 290 * 280 * 290 * 290	300 G NVPAGT S NVPAGT S NVPAGT S TPPAGT N TPPAGT N TPPAGT N TPPAGT A TPPAGT A TPPAGT T TPPAGT S TPAGT S	* * 310 (S DT VR V LT V (S DT VL VT VT V (S DT VL VT VS V (O D L S F VVE Y (O D L S F VVE Y (T D T LT VD VE F (S D L I VD VA F (S D L I VD VA F (S D L I VD VA F (S D V VL D VA F (T D VV L D VA F (S D V VL D VA F (S D V VL D VA F (S D VV VD VA F (S D VV VA F) (S D VV VA F (S D VV VA F) (S D VA F)
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_c1921/01-288 YP_1720/1-292 PP1Y_Mple92/1-301 Entas_2592/1-302 ETA_04540/1-307 PP14_34580/1-300 YE1856/1-302 PP14_3451/-301 PSEEN3394/1-301 H045_11530/1-304 M634_16375/1-302 PFL_3349/1-304 PAGR_07441/1-305 EbC_38210/1-306 ESA_01347/1-298 ROD_19341/1-301	230 - SGG - WR RM - SGG - WR RM - VG - WR QM - VA - WR QM - VA - WR RM - LNN - VR RM - LNN - VR RM - SGG - RR RMK S - GG - RR RMK S - GG - RR RMK S - GG - RR RMK 	240 * 250 256 ANA 10 YN LY KPG SST VGG	* 260 DSTVWTTSNTQAG OSTVWTASTDSA GSAWTESNNLSV STSRWGHLGTERRSSGE. TTVWDSTNKQSG STSRWGHLGTERRSSGE. TTNRWGSGTERWASA GPDWGDNGSARVFSA. GVRWGSGAARRSSTD. GVVRWGSLTTARRSSTD. GVVRWGSLTARRSSTD. GVVRWGSLTARRSSTD. STRWGSVGSARRSSTD. SSDRWGPSGTERVGSAA. TTTRWGPTGTDRVSSA TANRWGSVGSERWASSA	270 	280 * 290 * 280 * 290 * 280 * 290 * 200	300 G NVPAGT S NVPAGT S NVPAGT S TPPAGT N TPPAGT N TPPAGT N TPPAGT N TPPAGT A TPPAGT T TPPAGT S	* * 310 SDTVRVILTV SDTVLVTVS CODNLSFVVEY TODNLSFVVEY TODNLSFVEY SDTUVVVEY TOTLTVDVF SDTUVDVF SDTUVDVF SDSVILDVGF TDNVLDVGF TDNVLDVGF TDNVLDVGF TDNVLDVGF SDSVVDIAF SDSVVIDLSF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVLDVGF TDVVDVAF TDVVVDAF TDVVVDAF TDVVVDAF TDVVVDAF
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_e1921/01-288 YP_1720/1-292 PP1Y_Mple92/1-301 Enta_2592/1-302 ETA_04540/1-307 YE186/1-302 PP1W_31920/1-301 H045_11530/1-304 M634_16375/1-302 PPL_3349/1-304 PAGR_0744/1-305 EbC_38210/1-306 ESA_01347/1-288 ROD_19341/1-301 ECENIK_13825/1-302 Acav 45321/291	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VG - WR QM - VA - WR QM - L RI - RI - RR - SG - R RR MK S - GG - R RR MK S SG - R R RM S -	240 * 250 256 ANA 10 NL YKPG SSTVGGT - TRY L0Y0 IFKG SGP I ANOPT AWL0Y0 FY0PN NGT SNFMOY 01 VL PN CNGT SNFMOY 01 VL PN CNG SNY I AY EI YYPGG NA GSY I AY EI YYPGG SSA NNYL AY DI FKSA SSA SNYL AY DI FKSA SG SNYL AY DI FKSA SG SNYL AY DI FKSA SG SNYL AY DI FKSA SG SNYL SY EI YKSS SG SNRL SYE I YKAS SG	* 260 DSTVWTTSNTQAG OSTVWTASTDSSA GSAWTESNNLSV STSWGHLGTERRSSGE. TTVWOSGSTERWASSA GPDWGDNGSARVFSSA. GVDWGASGAARRSSTD. GVVRWGASGAARRSSTD. GVVRWGASGAARRSSTD. GAVRWGSLTTARRSSD. GTTRWGSVGARRSSTD. SSDRWGPSGTERWASA. TTRWGSVGSARRSSTD. SSDRWGPSGTERWSSA. TTNRWGSVGSERWASSA.	270 	280 * 290 * 280 * 290 * STAGNYPYRAIVNP-AD STSQSFPYTASVNL-AD STSQSFYTASVNL-AD STSQSFYTASVNL-AD STSQLIPYNAVINP-TO STQQLIPYNAVINP-OL STQQLIPYNAVINP-OL LTRTYNTAKULT-SD GSQUFNYNAKUYT-DD GSQUFNYNAKUYT-DD GSQUFNYNAKUYT-DD GSQUFNYNAKUYT-DD GSQUFNYNAKUYT-DD CSQUFNYNAKUYT-DD CSQUFNYNAKUYT-DD CSQUFNYNAKUYT-DD CSQUFNYNAKUYT-DD LTRSYNTARVLT-TD LTRSYNTARVLT-TD LTRSYNTARVLT-TD LLRTYNYTAKVLT-SD TPUVIPYTAKULT-SD TPUVIPYTARUS	300 S	* * 310 ISDTVRVILTY SDTVVTVTY YSDTVLVTVS YSDTVLVTVS YSDTVLVVSY YTDTLVDVF YSDTVVDSF YSDTVVDSF YSSVILDVGF YTDVVLDVGF YTDVVLDVGF YDSVLDVGF YDSVLDVGF YDSVVDJF YSSVVDJF YSSVVDJF YDSVVDJF YDTVVVDJF YDTVVVDJF YDTVVVDJF YDTVVVDJF YDTVVVDJF YDTVVDJF
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_e1921/01-288 YP_1720/1-292 PP1Y_Mple920/1-301 Entas_2592/1-302 ETA_04540/1-307 YP18_35/1-302 PP1W_312	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VG - WR QM - VA - WR QM - L NN - V R RM - L NN - V R RM - SGG - R R RMK S - GG - R R RMK S - GG - R R RMK S - GG - R R RMK 	240 * 250 256 ANA 10 NL YKPG SSTVGGT - TRY LOY 01 FK G SGP I ANOPT AWL 0Y 0F Y 0PN NGT SNFMOY 01 VL PN LT S GSY I AY E I Y VPG G- NG SNYMS DI YKEA TSG GNOLAY 01 YGGS SSA NNYL AY DI FK SA SSA NNYL AY DI FK SA SG SNYL AY DI FK SA SG	260 DSTWITTSNTQAG GSAWTESNNLAG GSAWTESNNLSV STSWGHLGTERRSSGE. TTVWOSGSTERWSSA GPDWGDNGSARVFSSA. GPDWGDNGSARVFSSA. GVDWGASGAARRSSTD. GVVRWGASGAARRSSTD. GVVRWGASGAARRSSTD. GAVRWGSLTTARRSSD. GTTRWGSVGARRSSTD. STRWGSVGARRSSTD. STRWGSVGARRSSTD. STRWGSVGARRSSTD. STRWGSVGARRSSTD. STRWGSVGARRSSTD. STRWGSVGARRSSTD. STRWGSVGARRSSTD. STRWGSVGSERWSSA. TTNRWGSVGSERWSSA. TTNRWGSSGERWSSA.	270 	280 * 290 * 280 * 290 * SAAONYPYRAIVNP-AD STSOSFPYTASVNL-AD STSOSFYTASVNL-AD STSOSFYTASVNL-AD STOOLIPYNAVINP-TO STOOLIPYNAVINP-OO STOOLIPYNAVINP-OO STOOLIPYNAVINP-OO SOVFNYNAKIVT-SO GSOVFNYNAKVYT-DD GSOVFNYNAKVYT-DD GSOVFNYNAKVYT-DD GSOVFNYNAKVYT-DD GSOVFNYNAKVYT-DD GSOVFNYNAKVYT-DD GSOVFNYNAKVYT-DD CSOVFNYNAKVYT-DD CSOVFNYNAKVYT-DD CSOVFNYNAKVYT-DD CSOVFNYNAKVYT-DD LTRSYNYTAKVLT-TD LTRSYNYTAKVLT-TD LTRSYNYTAKVLT-TD LTRYNYTAKVLT-SO TPIVLPYTAKVLT-SO TPIVLPYTARVLP-DD SSAOOFPYTARLYP-DD	300 300 S	* * 310 IS TVR VILT Y S TVL VTVY Y S TVL VTVS Y S TVL VTVS Y S TVL VVSY Y T TL VDVAF Y S SVL VVSY S S VL VVSY Y S SVL VVSY Y S SVV VVSY S S VVVD VSF Y S SVVVD VSY Y S SVVD VSY Y S SVVVD VSY Y S SVVD S SVVD S Y S SV S S Y S SV S S Y S SV S S Y S S S S S S S S S S S S S S S S S S S
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/288 YP_1720/1-292 PP1Y_Mpl692/1-301 Entas_2592/1-302 ETA_04540/1-307 YE186/1-302 PP1W_31920/1-301 H045_11530/1-304 M634_16975/1-302 PPL_3349/1-304 PPGR_0744/1-305 ESA_01347/1-288 ROD_19341/1-301 BMASAVP1_A1401/1-294 BPC006_11662/1-294 MDS_2712/1-298	230 - SGG - WR RM - SGG - WR QM - VG - WR QM - VG - WR QM - LG I R RL - L NN - V R RM - TG H - Q R YM - TG H - Q R YM - SGG - R R RMK S - GG - R R RMK S - GG - R R RMK S - GG - R R RMK - SGG - Q R M - SGG - Q R M - VG T - Q R YM - VG T - Q R YM - VG T - Q R YM - VG T - Q R M - SAG - R Q M - SAG - R Q M - SAG - R Q M - SAG - R Q M 	240 * 250 256 ANA 10 NL YKPG SSTVGGT - TRY LOY 0 IF K G. SOP I ANOPT AWL 0Y 0 F Y 0 PN KGT SNFMQY 0 1 YL PN LT S GSY I AY E I Y YPG G- NA GSY I AY E I Y YPG G- NG SNY MSY D I YK EA TSG GNULAY 0 IF KSA SSA NNY LAY D IF KSA SG SNY LAY D IF KSA SG SNY LAY D IF KSA SG	260 DSTVWTTSNTQAG GSAWTESNNLAG STSWTASTDSA STSWGHLGTERSSGE. TTVWOSGSGTERWSSA GPDWGDNGSARVFSSA. GPDWGDNGSARVFSSA. GVDWGASGAARRSSTD. GVVRWGASGAARRSSTD. GVVRWGSLTTARRASSD. GTVRWGSLTARRSSTD. GAVRWGSLTTARRASSD. STRWGSVGAARRASST. STRWGSVGAARRASST. TARWGVSGSERWSSA. TTRWGPTGTDRVSSA. TTNRWGSGSGAERWTSAT. TTNRWGSGSGAERWTSAT. TTNRWGSGSGAERWTSAT. SS-LWGTAGTRTAGT- AAAVWGGSANRAGSGA.	270 	280 * 290 * 280 * 290 * STAGNYPYRAIVNP-AD STSQSFPYTASVNL-AD STSQSFPYTASVNL-AD STSQSFPYTASVNL-AD STQQLIPYNAVINP-TO STQQLIPYNAVINP-OD STQQLIPYNAVINP-OD STQQLIPYNAVITAULT-SO GSQUFNYNAKVYT-DD GSQUFNYNAKVYT-DD GSQUFNYNAKVYT-DD GSQUFNYNAKVYT-DD GSQUFNYNAKVYT-DD CSQUFNYNAKVYT-DD CSQUFNYNAKVYT-DD SQUFNYNAKVYT-DD CSQUFNYNAKVYT-DD CSQUFNYNAKVYT-DD CSQUFNYNAKVYT-DD LTRSYNYTAKVLT-TD LTRSYNYTARVLT-TD LTRSYNYTARVLT-TD LTRSYNYTARVLT-TD LTRSYNYTARVLT-TD CSQQFYTARLYP-DD SSAQQFPYTARLYP-DD SSAQQFPYTARLYP-DD SSAQQFPYTARLYP-DD SSAQQFPYTARLYP-DD	300 S	* * 310 IS T VR VI LT V S T VL VT VT V YS T VL VT VS Y YO D NL S F VVE Y YO D NL S F VVE Y YO D NL S F VVE Y YO D VL S F V YO S VI LD VG F YS S VI LD VG F YS S VI LD VG F YD S VI D VG F YD S VV D LS F YT D T VVD LA F YT D T VVD LA F YT D T VVD LA F YT D S VVD LA F YT D S VVD VE Y YT D S VVD Y YT D S VVD VE Y YT D S VVD Y YT D S VD S S V YT D S VD S S S V YT D S S V D S S S S S S S S S S S S S S S
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/288 YP_1720/1-292 PP1Y_Mpl692/1-301 Enta_2592/1-302 ETA_04540/1-307 PP14_34580/1-300 YE186/1-302 PP14_34580/1-301 H045_11530/1-304 M634_16975/1-302 PPL_3349/1-304 PP4G_0744/1-305 EDC_38210/1-306 ESA_01347/1-288 ROD_19341/1-301 BMASAVP1_A1401/1-294 BPC006_11662/1-294 MDS_2712/1-298 YPC_2125/1-298	230 - SGG - WR RM SGG - WR QM VTG - WR QM LG I R RL LNN - VR RM TG H - Q YM S - GG - R R RMK VG T - Q R YM VG T - Q R YM VG T - Q R YM SAG - R QM S	240 * 250 256 ANA 10 NL YKPG SSTVGGT - TRYLOY 01 FK G. SOP I ANOPT AWLOY 0F Y0PN NA GSY I AY E I YVPG NA GSY I AY E I YVPG NA GSY I AY E I YVPG NG SNYMS D I YKE A TSG GNULAY 01 FKSA SSA NNYLAY D I FKSA SG SNYLAY D I FKSA SG SNYLAY D I FKSA SG SNYLAY D I FKSA SG SNRLSYE I YKGS SG ANRLAY D I FGPG NG ANRLAY D I FGPG SG SNFUNG	260 DSTVWTTSNTQAG GSAWTESNNLAG GSAWTESNNLSV STSRWGHLGTERRSSGE. TTVWOSGSGTERWSSA GPDWGDNGSARVFSSA. GPDWGDNGSARVFSSA. GVDWGASGAARRSSTD. GVVRWGASGAARRSSTD. GVVRWGSLTTARRASSD. GTVRWGSLTARRSSTD. GAVRWGSLTTARRASSD. GTTRWGSVGAARRSSTD. STRWGSVGAARRASST. TARWGVSGSERWSSA. TTRWGPTGTDRVSSA. TTRWGCSGAERWSSA. TTNRWGSGSGAERWSSA. TTNRWGSGSGAERWSSA. TTNRWGSGSGAERWSSA. TTNRWGSGSGAERWSSA. TTNRWGSGSGAERWSSA. TTNRWGSGSGAERWSSA. TTNRWGSGSGAERWSSA. SS. LWGTAAGTRTAGT- AAAVWGGSANRAGSGA. AAAVWGGSANRAGSGA.	270 	280 * 290 * SAAONVP YRA I VNP - AD STSOSFPYTASVNL - AD STSOSFYTASVNL - AD STAOSTANTLK I NP - TO SLAOSI PYTASVNL - AD STOOL I PYNAV I NP - OO STOOL I PYNAV I NP - OO STOOL I PYNAV I NP - OO SOVFNYNAK VYT - DO GSOVFNYNAKVYT - DO GSOVFNYNAKVYT - DO GSOVFNYNAKVYT - DO GSOVFNYNAKVYT - DO GSOVFNYNAKVYT - DO LTRSYNYTARVL - TO LTRSYNYTARVL - TO LTRSYNYTARVL - TO LTRSYNYTARVL - TO LTRSYNYTARVL - TO LTRSYNYTARVL - TO LTRSYNYTARVL - TO SAOOFPYTARLY - DO SSAOOFPYTARLY - DO	300 S NUP AGT S NUP AGT S NUP AGT S NUP AGT S TPPAGT N TPPAGT N TPPAGT N TPPAGT N TPPAGT A TPPAGT S TPPAGT S TPPAGT S TPPAGT S TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT A TPPAGT T TPPAGT A TPPAGT A TPPAGT T TPAGT A TPPAGT A TPPAGT T TPPAGT T TPAGT A TPPAGT T TPAGT T TP	* * 310 IS DTVR VILT Y S DTVVTVTY YS DTVLVTVS YS DTVLVTVS YS DTVLVTVS YS DTVLVTS YS DTVVE YS DTVVLS S TVTVDS YS DVVLDVG YS DVVLDVG YS DVVLDVG YD SVVLDVG YD SVVLDVG YD SVVLDVG YD SVVDVG YD SVVDVS YT DTVVVDIAF YT DTVVVDIAF YT DTVVVDIAF YT DSVVDVE YT DSVVD YT DSVD YT DSVD
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/282 PP1_7_01/92092/1-301 Entas_2592/1-302 ETA_04540/1-307 PP1_3000592/1-301 PP1_301/302 PP1_302/1-301 PSEEN3394/1-301 H045_11530/1-304 M634_16375/1-302 PPL_3349/1-304 PP4C_90744/1-305 ESA_01347/1-288 ROD_19341/1-301 BMASAVP1_A1401/1-294 BPC006_11652/1-294 MDS_2712/1-298 PC_2125/1-292 SWWW4, v1c21200/1-288 ECA3077/1-297	230 - SGG - WR RM SGG - WR QM VTG - WR QM LG I R RL LNN - V R RM CG - R RR MK S - GG - R R RMK S - GG - R R RMK S - GG - R R RMK S - SG - R R RMK S - SG - R R RMK S - SG - R R RMK S - GG - R R RMK S - GG - R R RMK	240 * 250	260 DSTVWTTSNTQAG GSXWTESNTQAG GSXWTESNNLSV STSRWGHLGTERRSSGE. TTVWOSGSGTERWSSA GPDWGDNGSARVFSSA. GPDWGDNGSARVFSSA. GPDWGDNGSARVFSSA. GVRWGASGAARRSSTD. GTVRWGASGAARRSSTD. GVRWGSLTTARRASSD. GTVRWGSLTARRSSTD. GTVRWGSLTARRSSTD. GTVRWGSLTARRSSTD. STRWGSVGAARRASST. TARWGSSGARRSSTD. SSDRWGPSGTERWSSA. TTRRWGVGSERWSSA. TTRRWGVGSERWSSA. TTRRWGVGSERWSSA. TTRRWGSGSGAERWTSAT. GS-LWGTAAGTRTAGT- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- SSLIWNAASPLTA GVLFWNVTNKRTS TTVWOSG	270 	** * 280 * 290 * SAA ONVP YRA I VNP - AD SAAONYP YRA I VNP - AD SAAONYP YRA I VNP - AD SAAONYP YRA I VNP - AD STAGS FPY TASYNL - AD STAGS FPY TASYNL - AD STAGS FPY TASYNL - AD STODL I PYNAV I NP - OD STODL I PYNAV I NP - OD STODL I PYNAV I NP - OD STODL I PYNAV I NP - OD STODL I PYNAV I NP - ND GSOV FNYNAK VYT - DD GSOV FNYNAK VYT - DD GSOV FNYNAK VYT - DD SGOV FNYNAK VYT - DD GSOV FNYNAK VYT - DD LTRYNYNAR I YT - DD LTRYNYT ARVLT - TD LLRYNYT ARVLT - TD LLRYNYT ARVLT - TD LLRYNYT ARVLT - TD LLRYNYT ARVLT - TD SAAOC PYTAR I VP - DD SSAGOF PYTAR VT TAR VLT - TD SAAOC FYTAR VLT - TD SAAOC FYTAR VLT - TD SSAGOF PYTAR VLT - TD SAAOC FYTAR VLT - DD SAAOC FYTAR VLT - DD SSAGOF PYTAR VLT - TD SAAOC FYTAR VLT - DD SAAOC FYTAR VLT - DD SSAOC FYTAR VLT - TD SAAOC FYTAR VLT - DD SAAOC FYTAR VLT - DD SSAOC FYTAR VLT AR VLT - DD SSAOC FYTAR VLT - DD SSAOC FYTAR VLT - DD SSAOC FYTAR VLT AR VLT - DD SSAOC FYTAR VLT - DD SSAOC FYTAR VLT - DD SSAOC FYTAR VLT AR V	300 G	* * 310 (S TV V V I V T V (S TV V V V V V Y (S TV V V V Y Y (S TV V V V S Y (S TV V V S Y (S T V V V S Y (S T V V V S Y (S T V V V S Y (S S V S Y (S S V S S Y (S S S V S S S S S S S S S S S S S S S S
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/288 YP_1720/1-292 PP1Y_Mple902/1-301 Entas_2592/1-302 ETA_04540/1-307 YP18_35/1-302 PP14_34580/1-300 YE186/1-302 PP14_34580/1-304 M634_16975/1-302 PPL_3349/1-304 PP4G_0744/1-305 ESA_01347/1-288 ROD_19341/1-301 BMASAVP1_A1401/1-294 BPC006_11662/1-294 MDS_2712/1-298 SMWW4, v1c21200/1-288 ECA3077/1-297 NGGM2_0934/1-291 CauE/1-312	230 - SGG - WR RM SGG - WR RM SGG - WR QM VTG - WR QM L NN - V R RM L NN - V R RM S - GG - R R RMK	240 * 250 250 - 250	260 DSTVWTTSNTQAG GSXWTESNTQAG GSXWTESNNLSV STSRWGHLGTERRSSGE. TTVWOSGSGTERWSSA. GPDWGDNGSARVFSSA. GPDWGDNGSARVFSSA. GPDWGDNGSARVFSSA. GTVRWGASGAARRSSTD. GSVRWGSLTTARRASSD. GTVRWGASGAARRSSTD. GTVRWGSLTARRASSD. GTVRWGSLTARRSSTD. GSVRWGSLTARRSSTD. GTVRWGSGAARRASST. TARWGSSGARRSSTD. SSDRWGSSGTERWSSA. TTRRWGVGSGERWSSA. TTRRWGVGSGERWSSA. TTRRWGSGSGAERWTSAT. GS-LWGTAAGTRTAGT- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- CSLIWNAASPLTA SSLIWNAASPLTA TTVWOTNKRTS TTVYNOTNKQGS NIAWTETNDYSG	270 	* * 280 * 290 * 280 Y 290 * 290 * 353 280 Y P 290 * 353 SSSSEPYTASYNL-AD S SSSSEPYTASYNL-AD 354 OSANYTLKINP-T0 SSAONYTLKINP-00 170011 PYNAXINP-00 SSTODLIPYNAVINP-00 17001YTYRAEILS SSOVFNYAKVYT-D0 SSOVFNYAKVYT-D0 GSOVFNYAKVYT-D0 GSOVFNYAKVYT-D0 SSOVFNYAKVYT-D0 GSOVFNYAKAVYT-D0 LIRSYNTARVLT-T0 LIRSYNTARVLT-T0 LIRSYNTARVLT-T0 LIRSYNTARVLT-T0 SSOSTFNYAKYT-D0 CSO FNYARITARVLT-T0 LIRSYNTARVLT-T0 LIRSYNTARVLT-T0 LIRSYNTARVLT-T0 SSAOOFPYTARLYP-D0 SSAOOFPYTARLYP SSAOOFPYTARLYP-D0 SSAOOFPYTARLYP-D0 SSAOOFPYTARLYP SSAOOFPYTARLYP-D0 SSAOOFPYTARLYP-D0 SLAOSIPYTARIANAAO SSAOOFPYTARLYP-D0 SSAOOFPYTARLYP-D0 SLAOSIPYTARIANAAO SSAOOFPYTARIANAAO SSAOOFPYTARIANAAO SITON IPYTARINA-SS SAAONYPYRAINAPAN SSAOONYPYR	300 S S NUPAGT S NOPAGT S NOPAGT S VADAGT S VADAGT S VADAGT S T PPAGT N PPAGT N PPAGT A T PPAGT A T PPAGT S T PPAGT T PPAGT A PPPGV P PPAGT A	* * 310 (S T V V V I V T V (S T V V V V V V Y (S T V V V V Y Y (T T V V V Y Y (T T V V Y Y Y Y (T T V V V Y Y Y (T T V V V Y Y Y (T T V V V V Y Y Y (T T V V V V Y Y Y (T T V V V V Y Y (T T V V V V Y Y Y (T T V V V Y Y Y (T T V V Y Y Y Y Y Y Y Y Y Y (T T V V Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y Y
PAM18_4750/1-291 Q7S_18315/1-296 KOX_23800/1-297 SOD_1292/01/288 YP_1720/1-292 PP1Y_Mpl0920/1-301 Entas_2592/1-302 ETA_04540/1-307 PP14_34580/1-300 YE1856/1-302 PP14_34580/1-300 PP14_34580/1-301 H045_11530/1-304 M634_16375/1-302 PPL_3349/1-304 PP4C_90744/1-305 EbC_38210/1-306 ESA_01347/1-288 ROD_19341/1-301 BMASAVP1_A1401/1-294 BPC006_11652/1-294 MD5_27121/298 SMWW4, v1c21200/1-288 ECA3077/1-297 NGGM2_0934/1-291 CsuE/1-312 BJAB0658_02454/1-312 BJAB0658_02454/1-312	230 - SGG - WR RM SGG - WR RM SGG - WR QM VTG - WR QM L 0	240 * 250 250 ANA 10 NL YKPG ST VGG TRY LOY 01 FKG. SOP I ANO PT AWL 0Y 0F Y0 PN NG SNFMOY 01 VL PN CLTS G. TDY LOY 01 VGGA NA OS YI AY EI YYPG G. NG SNYMS DI YKEA SG SNYMS DI YKEA SG SNYMS DI YKEA SG SNYL AY DI FKSA SG SNL AY DI FKSA SG SNL AY DI FKSA SG SNL SYE I YGS SG SNL SYE I YKS SG SNL SYE SG SNL SYE SG SNL SYE SG	260 DSTVWTTSNTQAG GSXWTESNTQAG GSXWTESNNQSG GSXWTESNNKQSG GTTVWQSGCTERWSSG GTVRWGGGTERWSSA GTDWGDNGSARVFSSA- GTURWGAGAARRSSTD. GTVRWGASGAARRSSTD. GTVRWGASGAARRSSTD. GTVRWGSLTTARRASSD. GTVRWGSLTARRASSD. GTRWGSVGAARRASST. STRWGSVGAARRASST. TARWGVSGTERWSSA. TTRWGSGGAERROSD GSTRWGSVGSERWSSA. TTRWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- AAAVWGQSANRAGSGA- NAAVTTSNTQAG STTVWDSTNKQSG NIAWTETNDYSG DSTWWTTSNTQAG SNDRWGS-GNERWSSLN.	270 	* * 280 280 280 280 280 280 280 280	300 G NVP AGT S NVP AGT S NVP AGT S NVP AGT S VP PAGT N VP PAGT N TP PAGT N TP PAGT N TP PAGT A TP PAGT A TP PAGT S TP PAGT S TP PAGT N TP PAGT T TP PAGT A TP PAGT T TP PAGT T TP PAGT A	* * 310 (S TV V V I V T V (S TV V V V V V V (S TV V V V V V V (S TV V V V V Y (S TV V V V E Y (S TV V V E Y (S S V V I L V Y (S S V V I L Y (S S V V I N Y (S S V Y I N Y (S S Y Y N Y (S S Y Y (S S Y
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_e1921/01-288 SVD_e1921/01-288 PT_1720/1-292 PT1V_Mpl692/1-301 Entas_2592/1-302 ETA_04540/1-307 PF1_3496/1-302 PF1_321/-301 PSEEN3394/1-301 PSEEN3394/1-301 PSEEN3394/1-301 PSEEN3394/1-304 PAGR_07441/-305 EbC_38210/1-306 ESA_01347/1-298 ROD_19341/1-301 BMASAVP1_A1401/1-294 BPC_091/1-291 BMASAVP1_A1401/1-294 BPC_005_17212 BMASAVP1_201 CauE/1-312 BJAB0868_02454/1-312 BJAB0868_0	230 - SGG - WR RM SGG - WR RM SGG - WR RM VTG - WR QM L QI R RL L NN - V R RM L NN - V R RM S - GG - R R RMK V T WR QM VG T - Q R YM	240 * 250 250 ANA 10 NL YKPG ST VGG TRY LOY 01 FK - G. SOP I ANOPT AWLOY 0F Y0PN - NG SNFMQY 01 YUPN - LT S - G - TD YLOY 0L Y0GA ANA GS YI AY EI YYPGG - SNYMS DI YKEA - TS GNOLAY 01 YGSS SNYMS DI YKEA - TS GNULAY 01 FKSA - SSA NNYLAY DI FKSA - SSA SNYLAY DI FKSA - SS SNYLAY DI FKSA - - SS TNA IO NLYYPA - SS TNA IO NLYYPA - SS TNA IO NLYYPA - SS TNA IO NLYYPA - SS SNYLAY - SNYLAY - SS SNYLAY - SNYLAY SNYLAY - SS SNYLAY S	260 DSTVWTTSNTQAG GSAWTESNNLAGG GSAWTESNNLSV STSRWGHLGTERRSSGE. TTVWOSGSGTERWSSA GPDWGDNGSARVFSSA GVRWGASGAARRSSTD. GVVRWGASGAARRSSTD. GVVRWGASGAARRSSTD. GTVRWGSLTTARRASSD. GTVRWGSLTARRASSD. GTVRWGSLTARRASSD. GTVRWGSLTARRASSD. GTTRWGSVGAARRASST. STRWGSVGAARRASST. TARWGVSGSERWSSA. TTRWGTTDRVSSA. TTRWGSGGAERRUSSA. TTRWGSGGAERWSSA. TTNRWGSGSGAERWSSA. TTRWGGSAARRASSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- SSLIWNAASPLTA SSLIWNAASPLTA SSLIWNAASPLTA SSLIWNAASPLTA SSLIWNASSCARWSSLN. SNDRWGS-GNERWSSLN.	270 	280 * 290 * SAAONYP YRA I VNP - AD STOSS FPYTASVNL - AD STOSS FPYTASVNL - AD STOSS FPYTASVNL - AD STOSS FPYTASVNL - AD STODI I PYNAV I NP - O STODI I PYNAV I NP - ND GSOV FNYNAKVYT - DD GSOV FNYNAKVYT - DD GSOV FNYNAKVYT - DD GSOV FNYNAKVYT - DD GSOV FNYNAKVYT - DD I TRYNYTAKVL T - TD LTRSYNYTARVL T - TD LTRSYNYTARVL T - TD LTRSYNYTARVL T - TD LTRSYNYTARVL T - DD SAOOF PYTARLY P SAOOF PYTARLY P SOOF STOVE P SAOOF PYTARLY P SAOOF PYTARLY P SAOOF PYTARLY P SAOOF PYTARLY P SOOF STOVE P SAOOF PYTARLY P SAOOF PYTARLY P SAOOF PYTARLY P SOOF STOVE P SO	300 G NVP AGT S NVP AGT S NVP AGT S NVP AGT S VPPAGT N TPPAGT N TPPAGT N TPPAGT N TPPAGT A TPPAGT A TPPAGT T TPPAGT S TPPAGT S TPPAGT N TPPAGT N TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT T TPPAGT A TPPAGT T TPPAGT T TPPAGT T TPPAGT T	* * 310 IS DTVR VILT Y S DTV VTVTY Y S DTV VTVTY Y S DTV VTVY Y S DTV VTVY Y S DTV VTVY Y S DTV VTV Y S DTV VDY Y S S VILDVGF Y S S VILDVGF Y S S VILDVGF Y S S VILDVGF Y S S VVID S S VVID S S VVID S S VVID Y S S S S S S S S S S S S S S S S S S S
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_c1921/01-288 SPD_c1921/01-288 PP117_Ubj6692/1-301 Entas_2592/1-302 ETA_04540/1-307 PP4_34580/1-300 PP4_34580/1-300 PP4_34580/1-301 PP4_513394/1-301 PF45_13394/1-301 PA65_11330/1-304 PA67_074/1-305 ESA_07347/1-298 ROD_19341/1-301 ESA_07347/1-298 ROD_19341/1-301 ESA_07347/1-298 PC06_1168271-294 BPC006_1168271-294 BPC066_1168271-294 BPC066_1168271-294 BPC066_1168271-294 BD5_27121/2-295 SMWW4_v1c21200/1-288 ECA307711-297 NCGM2_0934/1-291 CauE/1-312 BJAB0656_02454/1-312 BJAB0656_02454/1-316	230 - SGG - WR RM - SGG - WR RM - VG - WR QM - VG - WR QM - VA WR RM - L RI R RL - TG H - Q YM - TG H - Q YM - SG - R R RMK S - GG - R R RMK - VG Q YM - VG Q R M - VG Q R M - SG - R R QM 	240 * 250	260 DSTVWTTSNTQAG GSXWTESNTQAG GSXWTESNNQSG STSRWGHLGTERRSGE. TTVWOSGSGTERWSSG. GVRWGAGAGARRSSTD. GVVRWGAGAARRSSTD. GVVRWGAGAARRSSTD. GVVRWGSGAARRSSTD. GTVRWGSUTTARRASD. GTTRWGSVGAARRSSTD. GTVRWGSLTTARRASD. GTTRWGSVGAARRSSTD. SSDRWGSCGARRSSTD. SSDRWGSCGARRSSTD. GSTRWGSVGAARRASST. TTRRWGVGSGARRSSTD. SSDRWGSCGARRSSTD. GSTRWGSVGAARRASST. TTRRWGVGSGARRSSTD. SSDRWGSCGARRWSSA. TTRRWGVGSGARWSSA. TTNRWGSGGAERWJSAT. TTRRWGSGGAERWJSAT. GS-LWGTAAGTRTAGT- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- AAAVWGGSANRAGSGA- SSLIWNAASPLTA SVLIWNAASPLTA TTVWTTSNTQAG TTVWTTSNTQAG SNDRWGS-GNERWSSLN.	270 	* * 280 * 290 * SAA ONVP YRA I VNP - AD SAAONYP YRA I VNP - AD SAAONYP YRA I VNP - AD SAAONYP YRA I VNP - AD STAGS FPYTASYNL - AD STAGS FPYTASYNL - AD STAGS FPYTASYNL - AD STODI I PYNAY I NP - OD STODI I PYNAY I NP - AD STODI I PYNAY I NP - OD STODI I PYNAY I NP - OD STODI I PYNAY I NP - OD SGOV FNYNAK VYT - DD GSOV FNYNAK VYT - DD GSOV FNYNAK VYT - DD SGOV FNYNAK VYT - DD SGOV FNYNAK VYT - DD LTRYNYNAR I YT - DD LTRYNYNAR I YT - DD LTRYNYT ARVLT - TD LLRY YNTA RVLT - TD LLRYNYT ARVLT - TD LLRYNYT ARVLT - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAOOF PYTAR LYP - DD SSAONY PYRA I NP - AD STOONY PYRA I NP - AD STOONY PYRA I NP - AD STOONY PYR K I VDE NA SGONY PYRA I NP - AD SGONY PYRA I NP - AD SGONSTFVYG K I POGT SSAAKAHTYY	300 S S NUPAGT S NOPAGT S NOPAGT S NOPAGT S CKTGT S T	* * 310 (S DTV RV L T Y (S DTV VT VT Y (S DTV VT Y (S DTV VT Y (S DTV VT Y (S DTV VT Y (S DTV VT Y (S DTV YT Y (S DTV Y (S
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PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_c1921/01-288 YP_1720/1-292 PP11Y_Mp16692/1-301 Entas_2592/1-302 Ent_04540/1-307 PP4_34580/1-300 YE1856/1-302 Ppu_3322/1-301 P914_34580/1-304 PAG5_1030/1-304 M634_16975/1-302 PFL_3949/1-304 PAG5_0744/1-305 EbC_38210/1-306 EbC_38210/1-306 EbC_3821/1-291 BMASAVP_14701/1-298 BMASAVP_14701/1-294 BPC006_11682/1-294 MDS_2712/1-298 SMWW4_v1c21200/1-288 ECA397711-297 NCGM2_0347/1-291 PSG_50101-297 PSG_50101-297 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-298 PSG_55001-297 PSG_5	230 - S G - W R R - S G - W R R - V G - W R M - V G - W R M - V G - W R R - V R - W R R - V R - W R R - U N - V R R - U N - V R R - V T N - W R M - V T N - W R M - V T N - W R M - S G - R R R M K - S G - R R R M - S G - R R M - S G - S G - R R M - S G - R R M 	240 * 250 250 ANA 10 NL YKPG ST VGG - T TRY LOY 0 I K K - G. SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I ANO PT AWLOY 0 F Y 0 PN - SOP I PN - SOP I PN - SOP I PN -	260 DSTVWTTSNTQAG GSXWTESNTQAG GSXWTESNNTQAG GSXWTESNNKQSG GTVRWGASGATERSSGE. TTTVWDSTNKQSG GTVRWGASGATERSSGE. TNRKWGSGTERWSSA GDUWGDNGSARVPSSA GTUWGASGAARRSSTD. GTVRWGASGAARRSSTD. GTVRWGSGAARRSSTD. GTVRWGSLTTARRASSD. GTTRWGSVGAARRSSTD. GTVRWGSLTARRASSD. GTTRWGSVGAARRSSTD. GSTRWGSVGAARRSSTD. GSTRWGSVGAARRSSTD. SSDRWGSLTARRASSD. GSTRWGSVGAARRASST. TARRWGVSGTERWSSA. TTRWGOSGARRWTSAT. GS-LWGTAAGTRTAGT SSL WGTAAGTRTAGT SSL WGTAAGTRTAGT SSL WMASPLTA CVIPWNVTNKRTS TTVWDSTNKQSG TTVWDSTNKQSG TTTVWDSTNKQSG SSL WMASPLTA SVL WMASSL SSDRWGS-GNERWSSLN. SNDRWGS-GNERWSSLN. ATQRWGDWRSGD. YSTWDATGCVTNVGSS CTTSNRWGTIG SNDRWGS-GNERWSSLN.	270 	*** 200 280 * 280 * STAGNVPYKAIVNP-AD STSOSFPYTASVNL-AD STAGNVPYKAIVNP-AD STSOSFPYTASVNL-AD STAGNVTLKINP-TD SLAGSIPYKAIVN-AD STODIPYKAIVN-AD STODIPYKAIVN-AD STODIPYKAIVN-DD GSOVFNYNAKVYT-DD SGOVFNYNAKVYT-DD	300 G	* * 310 (S DTV RV L T Y (S DTV VT VT Y (S DTV VT VT Y (S DTV VT VT Y (S DTV VT VT Y (S DTV YT Y (S DTV Y (S DTV Y (S DTV Y
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PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_1212/101-288 YP_1720/1-292 PP1Y_Mpl692(1-301 Entas_2592/1-302 EntA_04540/1-307 PP4_34580/1-300 YE1856/1-302 Pp4_34580/1-300 YE1856/1-302 PP4_3495(1-302 PF4_349(1-304 PAGR_00744/1-305 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-306 EbC_38210/1-298 BMSAVP1_A1401/1-294 BPC006_11662/1-294 BMSAVP1_A1401/1-294 BPC086_02454/1-312 SAM048_02454/1-312 SAM048_02454/1-312 SAM048_02454/1-316 XAC1424/1-316 XAC1424/1-316 XAC1424/1-316 XAC1424/1-316 XAC1424/1-318 XAC1424/1-318 XAC1424/1-318 XAC1424/1-318 XAC1424/1-318 XAC14221/-295 BBK_506/1-296 Rta_34901-282 BT2_D0110/11-291	230 - S G - WR RM - S G - WR RM - VG D - WR QM - VG D - WR QM - VG P - WR RM - VA - WR RM - VA - WR RM - S - G - R R RM K - S - G - R R RM - S - G - R R RM - S - G - R R M - S - S	240 * 250 256 ANA 10 YN LY KPG AST VGG - TRY L0 YO IF K - G SG P I ANO PT AWL0 YO FY VO PN (NG T SNFMOY 0 I YU PN (LTS - G - TDY L0 YO I YU PN (LTS SNY I AY E I YP OG SA NNY LA YO IF KS A (LNSTT V - TDY L0 YO I YK EA SA NNY LA YO IF KS A (LNSTT V - TDY L0 YO I YK EA SA NNY LA YO IF KS A (LNSTT V - TDY L0 YO I YK EA SA NNY LA YO IF KS A SA		270 	280 * 290 * 280 Yean 290 * STAGNVPYKAIVNP-AD STAGNVPYKAIVNP-AD STAGNVPYKAIVNP-AD STAGNVPYKAIVNP-OD STAGNPYKAIVNP-OD STAGNPYKAIVNP-OD STAGNVPYKAIVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVNAKVYT-DD SGSOVFNVARAVIT-TD LLRTSYNTARVLT-TD LLRTSYNTARVLT-TD LLRTSYNTARVLT-TD LLRTSYNTARVLT-TD SGSAGPTYARLYD-DO LSSAGOFPYTARLYD-DO SSAGOFPYTARLYD-DO SSAGOFPYTARLYD-DO SSAGOFPYTARLYD-DO SSAGOFPYTARLYD-DO SSAGOFPYTARLYD-DO SSAGSTPYGAVANA-AD SGSAGSTPYGAVANA-AD SGSAGSTPYGAVANA-AD SITAOLITYNGEVPAOP-SSAAKHTVVYTWGRAPA-SO SAACHTVGEVPAOP-SSAAKHTVVYTWGRAPA-SD SITAOTTVTVGRAPA-SO SAACHTVGRVPAOT-SD SLODOPTTVGGVPAOT-SD SSASITVGGVPAOT-SD SUDOPTYMARAPA-AD SITAOTTVVGRAPA-AD SITAOTTVVGRAPA-AD SITAOTTVYGRAPA-AD	300 IG S NUPAGT S NOPAGT S NOPAGT S NOPAGT S NOPAGT S S NOPAGT T FPAGT N TPPAGT S T PPAGT S T PPAGT S T PPAGT S T PPAGT A PPAGT A PPPGV PPAGT A PPPGV PPAGT A QUANCYGT T PPAGT A SKFEGT G NVPAGT LSATGE SKFEGT SKFEGT LSATGE <td>* * 310 VS IV XVI UT Y VS TV VVI UT Y VS TV VVI VY Y VS TV VVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVVI Y VS VVVVI Y VS VVVVY VS VVVVY VS VVVVY VS VVVVY VS VVVY VS VVY VS VVVY VS VVVY VS VVVY VS VVVY VS VVVY VS VVVY VS VVY VS VS VVY V</td>	* * 310 VS IV XVI UT Y VS TV VVI UT Y VS TV VVI VY Y VS TV VVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVI Y VS VVVVI Y VS VVVVI Y VS VVVVY VS VVVVY VS VVVVY VS VVVVY VS VVVY VS VVY VS VVVY VS VVVY VS VVVY VS VVVY VS VVVY VS VVVY VS VVY VS VS VVY V
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PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_1921/01-288 YP_1720/1-292 PP1Y_Mple921/-301 Entas_2592/1-302 EntA_94540/1-307 PP4_34580/1-300 YE1856/1-302 Pp4_34580/1-300 YE1856/1-302 Pp4_34580/1-301 H045_11630/1-304 PF4_349/1-294 PF4_349/1-294 PF4_349/1-294 PF4_349/1-294 PF4_349/1-294 PF4_349/1-294 PF4_349/1-294 PF4_349/1-324 PF4_	230 - S GG - WR RM - S GG WR RM - VG D - WR QM - VG D - WR QM - VG - WR RM - VA - WR RM - L NN - VR RM - S GG - RR RMK S - GG - RR RMK S - GG - RR RMK S - GG - RR RMK - S GG - RR RM - S G - R QM - G S V - Q Q - G S V - G RM - G S V - G RM G S G S V - G RM G S G S V - G RM 	240 * 250 256 ANA 10 YN LY KPG SST VGG - TRY LO YO IF K - G SG P I ANO PT AWLO YO FY OP N (NG T SNFMOY OI YU PN (LTS - G - TDY LO YO IY PAG. YNG SSY I AY E IY YP OG. YNG SSY I AY E IY YP OG. YNG SSY I AY E IY YP OG. YNG SNYLAY D IF KS A (LNSTT V - TDY LO YO IY GA SSA NNYLAY D IF KS A (LNSTT V - TDY LO YO IY GA SSA NNYLAY D IF KS A SSA NNYLAY D IF KS A SSG SNELSY E IY KAS SG SNELSY E IY KAS SG NNRLSY E IY KAS SG NNRLSY E IY KAS SG NNRLOY D IF CPG SG NNRLOY D IF CPG SG NNAICO'N LF CPG SG NNAICO'N LF CPG SG NNAICO'N LF KNS NG ANRLOY D IF KNS NG NNYLOY U CUNTAG SG TDYLOY OL WRTG SG TDYLOY NLY NDA G FDYLOY CUNTAG G FDYLOY CUNAA. TG GG SWR OL Y DDA G FDYLOY CUNAA. TG GG SWR OL Y LDA GG NWN OL Y LDA GG NWN OL Y LDA 		270 	*** 200 280 *** 290 *** 290 *** 290 *** 290 *** 290 *** 290 *** 290 *** 290 *** 201 *** 201 *** 202 *** 203 PYLASVNL-AD 2040 PYLASVNL-AD 201 PYNAXVIT-NO 201 PYNYNAKVYT-DO 202 SQUYNYNAKVYT-DO 202 SQUYNNAKVYT-DO 202 SQUYNNAKVYT-DO 202 SQUYNNAKVYT-DO 202 SQUYNNAKVYT-DO 202 SQUYNNAKVYT-DO 202 SQUYNNAKVYT-DO 202 PYNARAVLTT 203 PYNARAVLT 203 PYNARAVLT 203 PYNARAVLT 203 PYNTARVLT 204 PYNTARVLT 205 PYNTARVLT <td>300 I S NUPAGT S NOPAGT S NOPAGT S NOPAGT S OKTYGT T NOPAGT S T PPGT T PPAT N T PPAGT S T PPAGT N T PPAGT N T PPAGT A PPAGT A PPAGT A PPPGV P PPAGT A PPPGV P PPAGT A PPPGV P PPAGT A SKPEGN VPAPGT LSAFGE <</td> <td>* * 310 VS DV VV U T Y VS DV VV U T Y VS DV VV VV Y VT DV VV Y VT DV VV VV Y VT DV VV VV Y VT DV VV Y VT DV VV VV Y VT DV VV Y VT TV VV Y VV Y VT TV VV Y VV Y VT TV VV Y VV Y</td>	300 I S NUPAGT S NOPAGT S NOPAGT S NOPAGT S OKTYGT T NOPAGT S T PPGT T PPAT N T PPAGT S T PPAGT N T PPAGT N T PPAGT A PPAGT A PPAGT A PPPGV P PPAGT A PPPGV P PPAGT A PPPGV P PPAGT A SKPEGN VPAPGT LSAFGE <	* * 310 VS DV VV U T Y VS DV VV U T Y VS DV VV VV Y VT DV VV Y VT DV VV VV Y VT DV VV VV Y VT DV VV Y VT DV VV VV Y VT DV VV Y VT TV VV Y VV Y VT TV VV Y VV Y VT TV VV Y VV Y
PAM18_4750/1-291 Q75_18315/1-296 KOX_23800/1-297 SOD_1921/01-288 YP_1720/1-292 PP1Y_M0[892/1-301 Entas_2592/1-302 EntA_94540/1-307 PP4_34580/1-300 PP4_34580/1-300 PP4_34580/1-300 PP4_34580/1-301 PP4_34580/1-301 PP4_34580/1-301 PP45_321/301 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-304 PF45_349/1-291 CauE/1-292 SMWW4_v1c21200/1-288 EC43077/1-297 PS5_56101-297 PS5_56101-297 PS5_56101-297 PS5_56101-297 PS75_57 PS75_57 PS	230 - S GG - WR RM - S GG WR RM - VG WR QM - VG WR QM - VG WR RM - L NN VR RM - T G H - Q R YM - S - GG - R R RMK - S - GG - R R RMK - S - GG - R R RMK - S - GG - R R RM - S - GG - R Q M - S - S - S - S 	240 * 250 256 ANA 10 YN LY KPG SST VGG - TRY LO YO IF K - G SG P I ANO PT AWLO YO FY OP N (NG T SNFMOY OI YU PN (LTS - G - TDY LO YO IY PAG. YNG SSY I AYE IY YP GG. YNG SSY I AYE IY YP GG. YNG SSY I AYE IY YP GG. YNG SNYLAY DI FKSA (LNSTT V - TDY LO YO I YKSA (LNSTT V - TDY LO YO I FKSA SSA NNYLAY DI FKSA SSG SNELSY EI YKAS SSG SNELSY EI YKAS SSG NNRLAY DI FKSA NG ANRLOY DI FCPG SSG OY IR NL YHNA SG TDYLOY OL YKTG SG DYLOY OL YKTG SG DYLOY OL YKTG SG		270 	*** 200 280 *** 290 *** 290 *** 290 *** 290 *** 290 *** 290 *** 290 *** 290 *** 290 *** 201 *** 201 *** 202 *** 203 PYLASVNLA 20401 PYNAXVIT 2050 *** 2041 PYNXAKVYT 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** 2050 *** <	300 I S NUPAGT S NOPAGT S NOPAGT S NOPAGT S NOPAGT T S S T T PPAT N T PPAT A T PPAGT S T PPAGT S T PPAGT S T S T PPAGT A PPPGV P T PPAGT A PPPGV P PPAGT A PPPGV P PPAGT A PPPQVGT P PPYPGV	* * 310 VS DIV RVI UT Y VS DIV RVI VS Y VS DIV RVI UT Y VS DIV RVI T VS DIV T VS

Alignment of two-domain tip subunits from archaic chaperone/usher (CU) systems. Sequences of two-domain subunits from archaic CU gene clusters were identified in various genomes (see the table bellow) and analyzed with the SignalP 4.1 server to detect and exclude secretion signal peptides. The predicted mature sequences were aligned with the program Clustal Omega at the EMBL-EBI website (10). The aligned sequences were edited and annotated using the program JalView (11). Conserved residues are color-coded according to their chemical properties: blue — hydrophobic, green — hydrophilic neutral, red — basic, magenta — acidic. Conserved cysteine residues are colored in pink. Glycine residues are shaded in orange, proline in yellow, aromatic residues in cyan. The sequences of two-domain subunits fall into families: the first family occupies the top part of the alignment table, above A. baumannii CsuE, (names of these sequences are shown in green), and the second family occupies the bottom part of the alignment table, below A. baumannii BJAB0868 02454 (names of these sequences are shown in blue). Completely invariant residues are indicated with an asterisk (*) in red and conserved positions containing less than 4% variable residues with an underlined asterisk (*) in red. Highly conserved regions (up to 15% variable residues) are marked with double dots (:) in red. Residues essential for semi-conservation (up to 25% non-matching residues) are dotted (.) in red. Conserved residues within each of the two families are indicated in a similar way, but the corresponding symbols are shown in green and blue for family 1 and 2, respectively. Secondary structure of the A. baumannii strain 19606 CsuE subunit (this paper) is shown above the alignment. Blue arrows and bars denote β strands and α helices, respectively.

#	Subunit name	Operon	Usher Accession	Chaperone Accession	Subunits Accession	Organism	Organism Class	Associated Disease	Operon DNA Accession
1	PAM18_4750	PAM18_4745 -4750	<u>AEO77229.1</u>	AE077228.1	AEO77230.1 AEO77227.1 AEO77226.1 AEO77225.1	Pseudomonas aeruginosa M18	γ Proteobacteria	Isolated from sweet melon rhizosphere	CP002496
2	Q7S_18315	Q7S_18290- 18315	AFE59873.1	<u>AFE59872.1</u>	AFE59874.1 AFE59871.1 AFE59870.1 AFE59869.1	Rahnella aquatilis HX2	y Proteobacteria	Isolated from a vineyard soil	CP003403
3	KOX_23800	KOX_23780- 23800	<u>AEX06475.1</u>	<u>AEX06474.1</u>	AEX06476.1 AEX06473.1 AEX06472.1	Klebsiella oxytoca KCTC 1686	γ Proteobacteria	Bacterium is used in production of 2,3- butylene glycol and 2,3-butanediol from xylose	CP003218
4	SOD_c19210	SOD_c19210 -c19260	<u>AGO54899.1</u>	AGO54900.1	AGO54901.1 AGO54902.1 AGO54903.1 AGO54898.1	Serratia plymuthica 4Rx13	y Proteobacteria	A plant-associated, plant beneficial bacterium	CP006250
5	YP_1720	YP_1720- 1725	<u>AAS61949.1</u>	<u>AAS61950.1</u>	AAS61951.1 AAS61952.1 AAS61953.1 AAS61948.1	Yersinia pestis biovar Microtus str. 91001	γ Proteobacteria	Causative agent of bubonic and pneumonic plague	AE017042
6	PP1Y_Mpl969 2	PP1Y_Mpl96 58-Mpl9692	CCA90809.1	CCA90808.1	CCA90807.1 CCA90806.1 CCA90810.1	Novosphingobiu m sp. PP1Y Mpl megaplasmid	α Proteobacteria	Isolated from a surface seawater sample collected from a closed bay	FR856861
7	Entas_2592	Entas_2592- 2596	<u>AEN65322.1</u>	<u>AEN65323.1</u>	AEN65324.1 AEN65325.1 AEN65321.1	Enterobacter asburiae LF7a	γ Proteobacteria	An opportunistic pathogen	CP003026
8	ETA_04540	ETA_04540- 04580	CAO95501.1	CAO95502.1	CAO95503.1 CAO95504.1 CAO95500.1	Erwinia tasmaniensis strain ET1/99	γ Proteobacteria	Non-phytopathogenic strain. Isolated from apple flowers.	CU468135
9	<i>PP</i> 4_34580	<i>PP</i> 4_34580- 34640	BAN55312.1	BAN55313.1	BAN55314.1 BAN55315.1 BAN55316.1	Pseudomonas putida NBRC 14164 DNA	γ Proteobacteria	Saprotrophytic soil bacterium	AP013070

Sequence source

					BAN55317.1				
			~		BAN55311.1			~	
10	YE1856	YE1856-1861	CAL11936.1	CAL11937.1	CAL11938.1	Yersinia	y Proteobacteria	Causes infections in	AM28641
					CAL11939.1	suhsp		lead to mild self-	5
					CAL11935.1	enterocolitica		limiting enterocolitis	
						8081		or terminal ileitis and	
								adenitis	
11	<i>Pput_3332</i>	Pput_3332-	ABQ79459.1	ABQ79460.1	ABQ79461.1	Pseudomonas	γ Proteobacteria	A versatile	CP000712
		3338			ABQ79462.1	putida F1		environmental isolate	
					ABQ/9463.1			that is capable of	
					ABQ79404.1 ABO79458.1			aromatic	
					ADQ77430.1			hvdrocarbons	
12	PSEEN3394	PSEEN3394-	CAK16145.1	CAK16146.1	CAK16147.1	Pseudomonas	y Proteobacteria	Entomopathogenic	CT573326
		3400			CAK16148.1	entomophila str.	•	bacterium which,	
					CAK16149.1	L48 chromosome		upon ingestion, kills	
					CAK16150.1			Drosophila	
12	110.45 11.620	110.45 116.20	ACE2(202.1	ACE2(202.1	CAK16144.1	Describences		melanogaster	CD004045
15	H045_11030	H045_11030- 11660	AGE20392.1	AGE20393.1	AGE20394.1	Pseudomonas	y Proteobacteria	hacterium shows	CP004045
		11000			AGE26396.1	poue RE 1-1-14		broad antagonistic	
					AGE26397.1			activity and is applied	
					AGE26391.1			to seeds as a	
								biocontrol agent to	
								suppress late root rot	
1.4	1624 16075	M(24 1(075	A C 002804 1	A C 002(17.1	A C 002(19.1	V:L		in the sugar beet	CD00(005
14	M034_109/3	M034_109/3 -16005	<u>AGQ93894.1</u>	AGQ92617.1	AGQ92618.1	V 10r10 parahaemolyticu	y Proteobacteria	A pathogenic marine	CP006005
		-10995			AGQ92019.1	s Ol·Kuk str		main causative agent	
					10001201011	FDA R31		of bacterial seafood-	
						chromosome II		borne gastroenteritis	
								in the United States	
15	PFL_3949	PFL_3955-	AAY93214.1	AAY93215.1	AAY93213.1	Pseudomonas	γ Proteobacteria	Pathogenic	CP000076
		3949			AAY93216.1	fluorescens Pf-5		bacterium, usually	
					AAY93217.1			affects patients with	
					AAY93219.2			immune systems	
16	PAGR g0744	PAGR g0744	AER31282.1	AER31283.1	AER31284.1	Pantoea	y Proteobacteria	Plant pathogen.	CP003085
_		-g0749			AER31285.1	ananatis PA13	,	Isolated from a	
		_			AER31280.1			diseased rice grain.	
17	EbC_ 38210	<i>EbC_38170-</i>	CAX61351.1	CAX61350.1	CAX61352.1	Erwinia	γ Proteobacteria	An epiphytic bacteria	FP236843
		38210			CAX61349.1	billingiae strain		and may represent	
					<u>CAX61348.1</u>	E0001		antagonists for	
								hlight	
18	ESA 01347	ESA 01343-	ABU76606.1	ABU76605.1	ABU76607.1	Cronobacter	y Proteobacteria	Human pathogen.	CP000783
	—	01347			ABU76604.1	sakazakii ATCC	•	Enterobacter	
					ABU76603.1	BAA-894		infection.	
19	ROD_19341	ROD_19341-	CBG88687.1	CBG88688.1	CBG88689.1	Citrobacter	γ Proteobacteria	Cause enteric disease	FN543502
		19381			CBG88690.1	rodentium		with a high rate of	
					CBU88080.1	100100		other rodents	
20	ECENHK 138	ECENHK 13	AFP70615.1	AFP70616.1	AFP70614.1	Enterobacter	y Proteobacteria	Nosocomial pathogen	CP003737
-	25	825-13845			AFP70618.1	cloacae subsp.	,	1	
						cloacae			
<u> </u>						ENHKU01	0.7	~	
21	Acav_4532	Acav_4528-	<u>ADX48414.1</u>	ADX48413.1	ADX48411.1	Acidovorax	β Proteobacteria	Causes seedling	CP002521
		4532			ADX48412.1	avenae subsp.		fruit blotch of	
					ADA40413.1	19860		cucurbits Under	
						12000		favorable	
								environment, it	
								becomes devastating	
								and may cause 100%	
								loss of marketable	
22	BMACAUDI 4	BMACAUDI	ABM52020 1	ABM52026 1	ABM52047 1	Buckhaldania	R Protochastoria	IIUIL.	CDUUUEDC
22	ымазатт_А 1401	A1395-	ADIVI32929.1	ADIVI32930.1	ABM50447 1	mallei SAVP1	ρ ε ι οιeovacieria	avirulent strain	CF000320
		A1401			ABM50929.1	chromosome I			
					ABM50824.1				

23	BPC006_1168 2	BPC006_116 77-11682	<u>AFR15557.1</u>	<u>AFR15556.1</u>	AFR15558.1 AFR15555.1 AFR15554.1 AFR15553.1	Burkholderia pseudomallei BPC006 chromosome I	β Proteobacteria	Isolated from a melioidosis patient	CP00378
24	MDS_2712	MDS_2707- 2712	<u>AEB58742.1</u>	<u>AEB58741.1</u>	AEB58743.1 AEB58740.1 AEB58739.1 AEB58738.1	Pseudomonas mendocina NK- 01	y Proteobacteria	Isolated from farmland soil	CP002620
25	YPC_2125	YPC_2119- 2125	ADV98708.1	ADV98707.1	ADV98710.1 ADV98706.1 ADV98705.1 ADV98704.1	Yersinia pestis biovar Medievalis str. Harbin 35	γ Proteobacteria	Causative agent of bubonic and pneumonic plague	CP001608
26	SMWW4_v1c2 1200	SMWW4_v1c 21200- v1c21250	AGE17922.1	AGE17923.1	AGE17924.1 AGE17925.1 AGE17926.1 AGE17921.1	Serratia marcescens WW4	γ Proteobacteria	A biofilm-forming bacterium isolated from paper machine aggregates	CP003959
27	ECA3077	ECA3073- 3076	<u>CAG75975.1</u>	<u>CAG75974.1</u>	CAG75972.1 CAG75973.1 CAG75976.1	Erwinia carotovora subsp. Atroseptica SCRI1043	γ Proteobacteria	Plant pathogenic bacterium, the causative agent of soft rot and blackleg potato diseases	BX950851
28	NCGM2_0934	NCGM2_093 4-0939	BAK87811.1	BAK87812.1	BAK87813.1 BAK87814.1 BAK87815.1 BAK87810.1	Pseudomonas aeruginosa NCGM2.SI DNA	γ Proteobacteria	The multidrug- resistant strain that caused an outbreak of urinary tract infection	AP012280
29	CsuE	Ab_Csu(A/B) ABCDE	<u>AAP43039.1</u>	<u>AAP43038.1</u>	AAP43035.1 AAP43036.1 AAP43037.1 AAP43040.1	Acinetobacter baumannii 19606	y Proteobacteria	Pneumonia, meningitis, septicemia, and urinary and respiratory tract infections in immuno- compromised individuals	AY24169 6
30	BJAB0868_02 454	BJAB0868_0 2454-02459	<u>AGQ11004.1</u>	AGQ11005.1	AGQ11006.1 AGQ11003.1 AGQ11008.1	Acinetobacter baumannii BJAB0868	γ Proteobacteria	Clinical isolate	CP003849
31	A3UG_03070	A3UG_0307 0-03085	<u>AFM58362.1</u>	<u>AFM58363.1</u>	AFM58364.1 AFM58361.1	Enterobacter cloacae subsp. dissolvens SDM	γ Proteobacteria	Isolated from soil samples	CP003678
32	P795_6510	P795_6495- 6510	<u>AHB91026.1</u>	<u>AHB91025.1</u>	AHB91027.1 AHB91024.1	Acinetobacter baumannii ZW85-1	γ Proteobacteria	Isolated from diarrheal patient feces	CP006768
33	<i>PSYCG_09745</i>	PSYCG_097 30-09745	<u>AGP49448.1</u>	<u>AGP49447.1</u>	AGP49449.1 <u>AGP49446.1</u>	Psychrobacter sp. G	γ Proteobacteria	Nonpathogenic soil bacterium, isolated from King George Island, Antarctica	CP006265
34	XCC1378	XCC1381- 1376	AAM40677.1	AAM40674.1 AAM40678.1	AAM40676.1 AAM40679.1	Xanthomonas campestris str. ATCC 33913	γ Proteobacteria	Causes a variety of plant disease	NC_00390 2
35	XAC1424	XAC1427- 1423	AAM36296.1	AAM36294.1 AAM36297.1	AAM36295.1 AAM36298.1	Xanthomonas axonopodis pv. citri str. 306	γ Proteobacteria	Exclusively pathogenic to a large group of plants such as citrus trees, rice, cotton, beans, and grapes	NC_00391 9
36	VAPA_1c2056 0	VAPA_1c205 60-1c20590	<u>AGU49161.1</u>	AGU49162.1	AGU49163.1 AGU49160.1	Variovorax paradoxus B4 chromosome 1	β Proteobacteria	Degrades the organic thiol compound mercaptosuccinate, which could be a promising precursor for novel polythioesters	CP003911
37	Sinme_6943	Sinme_6940- 6943	AEG58265.1	<u>AEG58264.1</u>	AEG58266.1 AEG58263.1	Sinorhizobium meliloti AK83 plasmid pSINME02	α Proteobacteria	Plant endosymbiont	CP002785
38	Bcep18194_A 5756	Bcep18194_ A5756- A5759	<u>ABB09353.1</u>	ABB09352.1	ABB09350.1 ABB09351.1	Burkholderia sp. 383 chromosome 1	β Proteobacteria	Isolated from forest soil	CP000151
39	Mesop 1922	Mesop 1919-	AEH86402.1	AEH86401.1	AEH86403.1	Mesorhizobium	a Proteobacteria	Isolated from B.	CP002279

		1922			AEH86400.1	opportunistum WSM2075		pelecinus plants	
40	BBK_506	BBK_506- 509	<u>AGZ27361.1</u>	<u>AGZ28430.1</u>	AGZ28097.1 AGZ29774.1	Burkholderia pseudomallei NCTC 13179 chromosome 1	β Proteobacteria	Human pathogen. Melioidosis.	CP003976
41	Rta_34890	Rta_34850- 34890	<u>AEG94601.1</u>	<u>AEG94600.1</u>	AEG94602.1 AEG94599.1	Ramlibacter tataouinensis TTB310	β Proteobacteria	Isolated in the Tatauoine meteorite in the desert of South Tunisia	CP000245
42	BYI23_D0121 10	BYI23_D012 120- D012150	<u>AET94722.1</u>	<u>AET94723.1</u>	AET94721.1 AET94724.1	Burkholderia sp. YI23 plasmid byi 1p	β Proteobacteria	Isolated from a golf course soil	CP003090
43	ABO_0699	ABO_0702- 0699	CAL16149.1	CAL16148.1	CAL16147.1 CAL16150.1	Alcanivorax borkumensis	γ Proteobacteria	Nonpathogenic marine bacterium	AM28669 0
44	BRPE64_DCD S03180	BRPE64_DC DS03190- 03210	BAN27255.1	BAN27256.1	BAN27257.1 BAN27254.1	Burkholderia sp. RPE64 plasmid p1 DNA	β Proteobacteria	Isolated from field- collected <i>Riptortus</i> pedestris	AP013061
45	AXYL_05495	AXYL_05492 -05495	ADP18794.1	ADP18793.1	ADP18792.1 Adp18795.1	Achromobacter xylosoxidans A8	β Proteobacteria	Isolated from soil contaminated with polychlorinated biphenyls.	CP002287
46	Smlt1510	Smlt1508- 1513	<u>CAQ45047.1</u>	<u>CAQ45048.1</u> <u>AQ45044.1</u>	<u>CAQ45049.1</u> <u>CAQ45046.1</u>	Stenotrophomon as maltophilia K279a	y Proteobacteria	Human pathogen isolated from a patient undergoing chemotherapy developed a bloodstream infection that did not respond to therapy with piperacillin/tazobacta m, ceftazidime or imipenem	AM74316 9
47	<i>OA238_c4625</i> <i>0</i>	OA238_c462 10-c46250	AGI74478.1	AGI74477.1	AGI74479.1 AGI74475.1	Octadecabacter arcticus 238	a Proteobacteria	Isolated from sea ice of the Arctic	CP003742 .1
48	Entcl_2278	Entcl_2275- 2278	ADO48529.1	ADO48528.1	ADO48527.1 ADO48530.1	Enterobacter lignolyticus SCF1	γ Proteobacteria	Isolated anaerobically from tropical forest soils	CP002272
49	XOO1979	XOO1982- 1978	<u>AAW75234.1</u>	AAW75232.1 AAW75235.1	AAW75233.1 AAW75236.1	Xanthomonas oryzae pv. oryzae KACC10331	γ Proteobacteria	Causes bacterial blight of rice	AE013598

Fig. S12

MNIKTKKLLRHLCMFSGLMLTGNMAHAACSVSASGTSSISVPSIYLMENGENSSQFNSGLSCTGF SLALANMTYLKYRVEQMSNSFTNAQTGEKLNAIILDSNNEIISLGQEKDMSSFTLVNLFSGPDGN LPFYIRLPAGQSVSPGVYQADSPLKVKWFYSVPAVAIVGIGVFFESPGFRRGALGIGFNWGSGAD SLGSLSITVLPDHHHHHH

Protein sequence of N-terminal domain of CsuE tagged with six histidine residues. Signal peptide and His₆-tag are shown in blue and green, respectively.

Fig. S13



Anti-CsuE antibody blocks Csu-pili mediated biofilm formation. *E.* coli/pBAD-Csu cells overexpressing Csu pili were preincubated with PBS buffer, 1:50 and 1:1000 dilutions of antibodies raised against the N-terminal domain of CsuE (αE_N) and CsuA/B ($\alpha A/B$) or the preimmune serum (S) and then assayed for biofilm formation in polystyrene microtiter plates. Biofilms were quantified by crystal violet staining and measuring absorbance at 595 nm. The results are representative of three independent experiments.





Csu pili are constitutively expressed and assembled on the cell surface of different *Acinetobacter baumannii* strains. Surface extracts prepared from *A. baumannii* strains 59798, 60611, 68164, 890, and 19069T from the Culture Collection of the University of Gothenburg (CCUG), lanes 1-5, respectively, and *E. coli* BL21 harboring pBAD-Csu in the presence (lane 6) and absence (lane 7) of arabinose, inducing Csu pili expression, were analyzed by Western blotting. The blot was probed with anti-CsuA/B rabbit serum followed by detection with IRDye 68RD-conjugated goat anti-rabbit antibody. The mobility of molecular mass markers is shown to the right in the figure.

Table S1.

Strains

Escherichia coli								
BL21-AI	<i>E. coli</i> str	<i>E.</i> coli strain B F ⁻ ompT gal dcm lon $hsdS_B(r_B m_B^-)$ $[malB^+]_{K-12}(\lambda^S)$						
	araB::T7RN	AP-tetA	1 0					
Acinetobacter ba	umannii							
Strain ^a	Source	Country	Year	Csu pili	Anti-CsuE serum			
		-		expression	dilution required for			
				level ^b	biofilm inhibition ^c			
CCUG 19096 T	Urine	France	1986	+++	1:1000			
CCUG 60611	Blood	Netherlands	1997	+++	1:1000			
CCUG 68164	Abdomen	Sweden	2006	++	1:1000			
CCUG 59798	Urine	Sweden	2010	+	1:1000			
CCUG 890	Urine	Great Britain	1970	+	1:1000			
0								

^a All strains were from the Culture Collection, University of Gothenburg (CCUG) ^b Estimated from the intensity of the band of CsuA/B in Western blots (Fig. S14) ^c Example of the experiment is shown in Fig. 4.

Table S2.

Oligonucleotides

Name	Sequence (5'→3')
CsuABABCDE_N-	AAGCGGCCGCAGATTAGCCATATTTTATTTGTCGAG
F	
CsuABABCDE_S-	TTGAGCTCTTAAAGATAAAAGCCCATGAACTGAG
R	
∆-CsuAB-R	GAATTCCGTTAATTCCTCCTGTTAG
Δ-CsuAB-F	GAGTAGCAGGTTTGCTCAAATATG
Δ-CsuA-R	TTAGAAATTTACAGTGACTAATAGAGTATC
Δ-CsuA-F	TAGTACCAATTACGATTGAGTTTTAAG
Δ-CsuB-R	TTTTCTTAAAACTCAATCGTAATTGGTAC
Δ-CsuB-F	ACGGCCGGAATTTATAAAGATACTG
Δ-CsuE-R	TCATGGCAAAGATACCTCGTGA
Δ-CsuE-F	TAAAAGCTGTTTTATATAGGAGATAAAAAG
CsuE-LALA_R	ACCCGAGCTAAAACCCGTACACGACAAAC
CsuE-LALA_F	TCAGGAAACATGACCTACCTAAAATATCGGGTTG
CsuE-IVGIGV_R	TCCCGAACTCGCGACTGCGGGCACAGAATAG
CsuE-IVGIGV_F	AGCGGGTCGTTCTTTGAGAGTCCTGGGTTTAG
CsuE-LGI_R	CCAATGCACCGCGTCTAAACCCAGG
CsuE-LGI_F	GTATTGGTTTTAACTGGGGAAGTGGGGC
CsuEN6Hrev	GTGATGATGAAGTACGGTAATTGAGAGTGAAC
CsuEN6Hfwd	CATCACCATTAATGAAAGGGCGAGCTC
CsuE-N6H_PR	TGGAAGTACGGTAATTGAGAGTGAAC
CsuE-N6H_DF	GACCATCATCACCATCACCATTAATG

Table S3

Refinement statistics

itennement statistics	
Data set	Native data
Resolution	53.9-2.31
Number of reflections	
- Total	87930
- Work set	83189
- Test set	4741
$R_{\text{work}}/R_{\text{free}}$ (%)	21.18/25.87
Number of atoms	
- Protein	7688
- Solvent	178
Number of protein	1000
residues	
Number of modified	6 (N-dimethyllysine) ^a
residues	
Number of ligands/ions	0
Wilson B-factor (Å ²)	54.01
Average B-factor (Å ²)	
- Main chain	65.77
- Side chain	78.15
- Solvent	55.20
Rmsd stereochemistry	
- Bond lengths (Å)	0.0043
- Bond angles (°)	1.050
Rmsd B-factors	
- Main chain	4.106
- Side chain	4.982
Ramachandran analysis ^b	
Residues in outlier regions	0.73%
Residues in favored regions	95.7%
Residues in allowed regions	99.27%

^a Methylated lysine residues ^b Output from Molprobity (outliers motivated by electron density)

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